



SEQUENCE LISTING

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<120> Process for preparing ketocarotenoids in genetically modified organisms

<130> 13173-00006-US

<140> US 10/524,827

<141> 2005-02-18

<150> PCT/EP2003/009106

<151> 2003-08-18

<150> DE 102 38 980.2

<151> 2002-08-20

<150> DE 102 38 978.0

<151> 2002-08-20

<150> DE 102 38 979.9

<151> 2002-08-20

<150> DE 102 53 112.9

<151> 2002-11-13

<150> DE 102 58 971.2

<151> 2002-12-16

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<170> PatentIn version 3.4

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Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu	
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gat tta ttg aaa aaa cat tgg tta cac cac gga cat cct ggt act gat Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp 115 120 125	384
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aat aat tta att ata ttt tgg atg ata cct tct att tta agt tca gta Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val 180 185 190	576
caa cta ttt tat ttt ggt aca ttt ttg cct cat aaa aag cta gaa ggt Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly 195 200 205	624
ggt tat act aac ccc cat tgt gcg cgc agt atc cca tta cct ctt ttt Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe 210 215 220	672
tgg tct ttt gtt act tgt tat cac ttc ggc tac cac aag gaa cat cac Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His 225 230 235 240	720
gaa tac cct caa ctt cct tgg tgg aaa tta cct gaa gct cac aaa ata Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile 245 250 255	768
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 35 40 45
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 50 55 60
 Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 65 70 75 80
 Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
 85 90 95
 Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
 100 105 110
 Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
 115 120 125
 Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp
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 Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly
 145 150 155 160
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 165 170 175
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 180 185 190
 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly
 195 200 205
 Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe
 210 215 220
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 65 70 75 80
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 Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
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 Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
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 aat cat tgc tta cat cat cgt cat cct gct agc gaa gtt gac cca gat 384
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 115 120 125
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 Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
 130 135 140
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 Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu
 145 150 155 160
 ttt aat tta gct aaa tac gtt ttg cac atc cat caa ata aat ctc atc 528
 Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
 165 170 175
 tta ttt tgg agt att cct cca att tta agt tcc att caa ctg ttt tat 576
 Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
 180 185 190
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 Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr

195	200	205	
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Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile			
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Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His			
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gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac			768
Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn			
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 Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
 50 55 60
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 115 120 125
 Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
 130 135 140
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 145 150 155 160
 Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
 165 170 175
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 180 185 190

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
 195 200 205

Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
 210 215 220

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
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 Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
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 Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp
 35 40 45
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 Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
 50 55 60
 aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat 240
 Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
 65 70 75 80
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 Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
 85 90 95
 ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa 336
 Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys
 100 105 110
 aaa cat tgg tta cac cac cac aat cca gca agc tca ata gac ccg gat 384
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 115 120 125

ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt 432
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135

140

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tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act 528
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180 185 190

ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag 624
Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln
195 200 205

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210 215 220

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35 40 45

Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
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Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
85 90 95

Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys
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 Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp
 115 120 125
 Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe
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 Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr
 165 170 175
 Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr
 180 185 190
 Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln
 195 200 205
 Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile
 210 215 220
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 Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn
 35 40 45
 tat gcc aaa att cat aag tgg ttg ata cct att gca ata gtt tgg caa 192
 Tyr Ala Lys Ile His Lys Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
 50 55 60
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Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys	100	105	110	
aat cat tgc tta cat cat cgt cat cct gct agc gaa gtt gac cca gat				384
Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp	115	120	125	
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Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe	130	135	140	
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Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu	145	150	155	160
ttt aat tta gct aaa tac gtt ttg cac atc cat caa ata aat ctc atc				528
Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile	165	170	175	
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ttc gga aca ttt ttg cct cat cga gaa ccc aag aaa gga tat gtt tat				624
Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr	195	200	205	
ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc				672
Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile	210	215	220	
gct tgc tac cac ttt ggt tat cat gaa gaa cat cat gag tat ccc cat				720
Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His	225	230	235	240
gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac				768
Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn	245	250	255	
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Ile	Ile	Ser	Leu	Trp	Val	Ala	Ser	Leu	Ala	Phe	Leu	Leu	Ala	Ile	Asn
		35					40					45			
Tyr	Ala	Lys	Ile	His	Lys	Trp	Leu	Ile	Pro	Ile	Ala	Ile	Val	Trp	Gln
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145					150					155				160	
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Leu	Phe	Trp	Ser	Ile	Pro	Pro	Ile	Leu	Ser	Ser	Ile	Gln	Leu	Phe	Tyr
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	210					215					220				
Ala	Cys	Tyr	His	Phe	Gly	Tyr	His	Glu	Glu	His	His	Glu	Tyr	Pro	His
225					230					235				240	
Val	Pro	Trp	Trp	Gln	Leu	Pro	Ser	Val	Tyr	Lys	Gln	Arg	Val	Phe	Asn
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<223> Artificial sequence

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1				5				10					15			

tta	agt	gct	aaa	gaa	gat	act	ggt	tgg	ggg	ctg	gtg	att	gtc	ata	gta	96
Leu	Ser	Ala	Lys	Glu	Asp	Thr	Val	Trp	Gly	Leu	Val	Ile	Val	Ile	Val	
			20					25					30			

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Ile	Ile	Ser	Leu	Trp	Val	Ala	Ser	Leu	Ala	Phe	Leu	Leu	Ala	Ile	Asn	
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Tyr	Ala	Lys	Val	Pro	Ile	Trp	Leu	Ile	Pro	Ile	Ala	Ile	Val	Trp	Gln	
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Gly	Ser	Val	Tyr	Arg	Lys	Asn	Pro	Lys	Ile	Asn	Asn	Phe	Ile	Gly	Ser	
				85				90					95			

cta	gct	gta	gcg	ctt	tac	gct	gtg	ttt	cca	tat	caa	cag	atg	tta	aag	336
Leu	Ala	Val	Ala	Leu	Tyr	Ala	Val	Phe	Pro	Tyr	Gln	Gln	Met	Leu	Lys	
			100					105					110			

aat	cat	tgc	tta	cat	cat	cgt	cat	cct	gct	agc	gat	tta	gac	cca	gat	384
Asn	His	Cys	Leu	His	His	Arg	His	Pro	Ala	Ser	Asp	Leu	Asp	Pro	Asp	
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Phe	His	Asp	Gly	Lys	Arg	Thr	Asn	Ala	Ile	Phe	Trp	Tyr	Leu	His	Phe	
	130					135					140					

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145					150				155					160		

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Phe	Asn	Leu	Ala	Lys	Tyr	Val	Leu	His	Ile	His	Gln	Ile	Asn	Leu	Ile	
				165				170						175		

tta	ttt	tgg	agt	att	cct	cca	att	tta	agt	tcc	att	caa	ctg	ttt	tat	576
Leu	Phe	Trp	Ser	Ile	Pro	Pro	Ile	Leu	Ser	Ser	Ile	Gln	Leu	Phe	Tyr	
			180					185					190			

ttc	gga	aca	ttt	ttg	cct	cat	cga	gaa	ccc	aag	aaa	gga	tat	ggt	tat	624
Phe	Gly	Thr	Phe	Leu	Pro	His	Arg	Glu	Pro	Lys	Lys	Gly	Tyr	Val	Tyr	

195	200	205	
ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc			672
Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile			
210	215	220	
gct tgc tac cac ttt ggt tat cat gaa gaa cat cat gag tat ccc cat			720
Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His			
225	230	235	240
gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac			768
Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn			
245	250	255	
aat tca gta acc aat tcg taa			789
Asn Ser Val Thr Asn Ser			
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<210> 10
 <211> 262
 <212> PRT
 <213> Unknown

<220>
 <223> Artificial sequence

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 Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val
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 Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn
 35 40 45
 Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
 50 55 60
 Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His
 65 70 75 80
 Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
 85 90 95
 Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
 100 105 110
 Asn His Cys Leu His His Arg His Pro Ala Ser Asp Leu Asp Pro Asp
 115 120 125
 Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
 130 135 140
 Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu
 145 150 155 160

Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
 165 170 175
 Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
 180 185 190
 Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
 195 200 205
 Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
 210 215 220
 Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
 225 230 235 240
 Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn
 245 250 255
 Asn Ser Val Thr Asn Ser
 260

<210> 11
 <211> 762
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <223> Artificial sequence

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 gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc 96
 Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
 20 25 30
 att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac 144
 Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp
 35 40 45
 atc tca aag att cat aag tgg atg tta ttg cct gtt ata cta tgg caa 192
 Ile Ser Lys Ile His Lys Trp Met Leu Leu Pro Val Ile Leu Trp Gln
 50 55 60
 aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat 240
 Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
 65 70 75 80
 ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca 288
 Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
 85 90 95
 ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa 336

Leu	Thr	Leu	Ser	Leu	Tyr	Gly	Leu	Leu	Pro	Tyr	Gln	Lys	Leu	Leu	Lys	
			100					105					110			
aaa	cat	tgg	tta	cac	cac	cac	aat	cca	gca	agc	tca	ata	gac	ccg	gat	384
Lys	His	Trp	Leu	His	His	His	Asn	Pro	Ala	Ser	Ser	Ile	Asp	Pro	Asp	
		115					120					125				
ttt	cac	aat	ggt	aaa	cac	caa	agt	ttc	ttt	gct	tgg	tat	ttt	cat	ttt	432
Phe	His	Asn	Gly	Lys	His	Gln	Ser	Phe	Phe	Ala	Trp	Tyr	Phe	His	Phe	
	130					135					140					
atg	aaa	ggt	tac	tgg	agt	tgg	ggg	caa	ata	att	gcg	ttg	act	att	att	480
Met	Lys	Gly	Tyr	Trp	Ser	Trp	Gly	Gln	Ile	Ile	Ala	Leu	Thr	Ile	Ile	
	145				150					155					160	
tat	aac	ttt	gct	aaa	tac	ata	ctc	cat	atc	cca	agt	gat	aat	cta	act	528
Tyr	Asn	Phe	Ala	Lys	Tyr	Ile	Leu	His	Ile	Pro	Ser	Asp	Asn	Leu	Thr	
				165					170					175		
tac	ttt	tgg	gtg	cta	ccc	tcg	ctt	tta	agt	tca	tta	caa	tta	ttc	tat	576
Tyr	Phe	Trp	Val	Leu	Pro	Ser	Leu	Leu	Ser	Ser	Leu	Gln	Leu	Phe	Tyr	
			180					185					190			
ttt	ggt	act	ttt	tta	ccc	cat	agt	gaa	cca	ata	ggg	ggt	tat	gtt	cag	624
Phe	Gly	Thr	Phe	Leu	Pro	His	Ser	Glu	Pro	Ile	Gly	Gly	Tyr	Val	Gln	
		195					200					205				
cct	cat	tgt	gcc	caa	aca	att	agc	cgt	cct	att	tgg	tgg	tca	ttt	atc	672
Pro	His	Cys	Ala	Gln	Thr	Ile	Ser	Arg	Pro	Ile	Trp	Trp	Ser	Phe	Ile	
		210				215					220					
acg	tgc	tat	cat	ttt	ggc	tac	cac	gag	gaa	cat	cac	gaa	tat	cct	cat	720
Thr	Cys	Tyr	His	Phe	Gly	Tyr	His	Glu	Glu	His	His	Glu	Tyr	Pro	His	
	225				230					235					240	
att	tct	tgg	tgg	cag	tta	cca	gaa	att	tac	aaa	gca	aaa	tag			762
Ile	Ser	Trp	Trp	Gln	Leu	Pro	Glu	Ile	Tyr	Lys	Ala	Lys				
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 <211> 253
 <212> .PRT
 <213> Unknown

<220>
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<400> 12

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Val	Leu	Arg	Ser	Lys	Ser	Gln	Phe	Lys	Gly	Leu	Phe	Ile	Ala	Ile	Val	
			20					25					30			
Ile	Val	Ser	Ala	Trp	Val	Ile	Ser	Leu	Ser	Leu	Leu	Leu	Ser	Leu	Asp	
		35					40					45				

Ile Ser Lys Ile His Lys Trp Met Leu Leu Pro Val Ile Leu Trp Gln
 50 55 60
 Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
 65 70 75 80
 Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
 85 90 95
 Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys
 100 105 110
 Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp
 115 120 125
 Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe
 130 135 140
 Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile
 145 150 155 160
 Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr
 165 170 175
 Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr
 180 185 190
 Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln
 195 200 205
 Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile
 210 215 220
 Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
 225 230 235 240
 Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys
 245 250

<210> 13
 <211> 762
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <223> Artificial sequence

<400> 13

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gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc 96
 Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
 20 25 30

att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp 35 40 45	144
atc tca aag cta aaa ttt tgg atg tta ttg cct gtt ata cta tgg caa Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln 50 55 60	192
aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His 65 70 75 80	240
ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr 85 90 95	288
ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys 100 105 110	336
aaa cat tgg tta cac cac cac aat cca gca agc gat tta gac ccg gat Lys His Trp Leu His His His Asn Pro Ala Ser Asp Leu Asp Pro Asp 115 120 125	384
ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe 130 135 140	432
atg aaa ggt tac tgg agt tgg ggg caa ata att gcg ttg act att att Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile 145 150 155 160	480
tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr 165 170 175	528
tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta caa tta ttc tat Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr 180 185 190	576
ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln 195 200 205	624
cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile 210 215 220	672
acg tgc tat cat ttt ggc tac cac gag gaa cat cac gaa tat cct cat Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His 225 230 235 240	720
att tct tgg tgg cag tta cca gaa att tac aaa gca aaa tag Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys 245 250	762

<211> 253
 <212> PRT
 <213> Unknown

<220>
 <223> Artificial sequence

<400> 14

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          20           25           30

Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp
          35           40           45

Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
          50           55           60

Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
65           70           75           80

Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
          85           90           95

Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys
          100          105          110

Lys His Trp Leu His His His Asn Pro Ala Ser Asp Leu Asp Pro Asp
          115          120          125

Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe
          130          135          140

Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile
145          150          155          160

Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr
          165          170          175

Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr
          180          185          190

Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln
          195          200          205

Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile
          210          215          220

Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
225          230          235          240

Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys
          245          250

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<210> 15

<211> 1608
 <212> DNA
 <213> Haematococcus pluvialis

<220>
 <221> CDS
 <222> (3)..(971)

<400> 15

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ggc cca cct cct cat ctc cat cgg tca ttt gct gct acc acg atg ctg	95
Gly Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu	
20 25 30	
tcg aag ctg cag tca atc agc gtc aag gcc cgc cgc gtt gaa cta gcc	143
Ser Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala	
35 40 45	
cgc gac atc acg cgg ccc aaa gtc tgc ctg cat gct cag cgg tgc tcg	191
Arg Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser	
50 55 60	
tta gtt cgg ctg cga gtg gca gca cca cag aca gag gag gcg ctg gga	239
Leu Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly	
65 70 75	
acc gtg cag gct gcc ggc gcg ggc gat gag cac agc gcc gat gta gca	287
Thr Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala	
80 85 90 95	
ctc cag cag ctt gac cgg gct atc gca gag cgt cgt gcc cgg cgc aaa	335
Leu Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys	
100 105 110	
cgg gag cag ctg tca tac cag gct gcc gcc att gca gca tca att ggc	383
Arg Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly	
115 120 125	
gtg tca ggc att gcc atc ttc gcc acc tac ctg aga ttt gcc atg cac	431
Val Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His	
130 135 140	
atg acc gtg ggc ggc gca gtg cca tgg ggt gaa gtg gct ggc act ctc	479
Met Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu	
145 150 155	
ctc ttg gtg gtt ggt ggc gcg ctc ggc atg gag atg tat gcc cgc tat	527
Leu Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr	
160 165 170 175	
gca cac aaa gcc atc tgg cat gag tcg cct ctg ggc tgg ctg ctg cac	575
Ala His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His	
180 185 190	
aag agc cac cac aca cct cgc act gga ccc ttt gaa gcc aac gac ttg	623
Lys Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu	

195	200	205	
ttt gca atc atc aat gga ctg ccc gcc atg ctc ctg tgt acc ttt ggc Phe Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly 210 215 220			671
ttc tgg ctg ccc aac gtc ctg ggg gcg gcc tgc ttt gga gcg ggg ctg Phe Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu 225 230 235			719
ggc atc acg cta tac ggc atg gca tat atg ttt gta cac gat ggc ctg Gly Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu 240 245 250 255			767
gtg cac agg cgc ttt ccc acc ggg ccc atc gct ggc ctg ccc tac atg Val His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met 260 265 270			815
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ggc gcg ccc tgg ggt atg ttc ttg ggt cca cag gag ctg cag cac att Gly Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile 290 295 300			911
cca ggt gcg gcg gag gag gtg gag cga ctg gtc ctg gaa ctg gac tgg Pro Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp 305 310 315			959
tcc aag cgg tag ggtgcggaac caggcacgct ggtttcacac ctcatgcctg Ser Lys Arg 320			1011
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cacatcatca tgtgcggttg gaggggctgg cacagtgtgg gctgaactgg agcagttgtc			1191
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gtgcagcaaa ctatattcac ctagggtgtg ttgtaggatac aggtgaggcc ttgcacattg			1371
catgatgtac tcgtcatggt gtgttggtga gaggatggat gtggatggat gtgtattctc			1431
agacgtagac cttgactgga ggcttgatcg agagagtggg ccgtattctt tgagagggga			1491
ggctcgtgcc agaaatggtg agtggatgac tgtgacgctg tacattgcag gcagggtgaga			1551
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<210> 16

<211> 322

<212> PRT

<213> Haematococcus pluvialis

<400> 16

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Lys	Leu	Gln	Ser	Ile	Ser	Val	Lys	Ala	Arg	Arg	Val	Glu	Leu	Ala	Arg	35	40	45	
Asp	Ile	Thr	Arg	Pro	Lys	Val	Cys	Leu	His	Ala	Gln	Arg	Cys	Ser	Leu	50	55	60	
Val	Arg	Leu	Arg	Val	Ala	Ala	Pro	Gln	Thr	Glu	Glu	Ala	Leu	Gly	Thr	65	70	75	80
Val	Gln	Ala	Ala	Gly	Ala	Gly	Asp	Glu	His	Ser	Ala	Asp	Val	Ala	Leu	85	90	95	
Gln	Gln	Leu	Asp	Arg	Ala	Ile	Ala	Glu	Arg	Arg	Ala	Arg	Arg	Lys	Arg	100	105	110	
Glu	Gln	Leu	Ser	Tyr	Gln	Ala	Ala	Ala	Ile	Ala	Ala	Ser	Ile	Gly	Val	115	120	125	
Ser	Gly	Ile	Ala	Ile	Phe	Ala	Thr	Tyr	Leu	Arg	Phe	Ala	Met	His	Met	130	135	140	
Thr	Val	Gly	Gly	Ala	Val	Pro	Trp	Gly	Glu	Val	Ala	Gly	Thr	Leu	Leu	145	150	155	160
Leu	Val	Val	Gly	Gly	Ala	Leu	Gly	Met	Glu	Met	Tyr	Ala	Arg	Tyr	Ala	165	170	175	
His	Lys	Ala	Ile	Trp	His	Glu	Ser	Pro	Leu	Gly	Trp	Leu	Leu	His	Lys	180	185	190	
Ser	His	His	Thr	Pro	Arg	Thr	Gly	Pro	Phe	Glu	Ala	Asn	Asp	Leu	Phe	195	200	205	
Ala	Ile	Ile	Asn	Gly	Leu	Pro	Ala	Met	Leu	Leu	Cys	Thr	Phe	Gly	Phe	210	215	220	
Trp	Leu	Pro	Asn	Val	Leu	Gly	Ala	Ala	Cys	Phe	Gly	Ala	Gly	Leu	Gly	225	230	235	240
Ile	Thr	Leu	Tyr	Gly	Met	Ala	Tyr	Met	Phe	Val	His	Asp	Gly	Leu	Val	245	250	255	
His	Arg	Arg	Phe	Pro	Thr	Gly	Pro	Ile	Ala	Gly	Leu	Pro	Tyr	Met	Lys	260	265	270	
Arg	Leu	Thr	Val	Ala	His	Gln	Leu	His	His	Ser	Gly	Lys	Tyr	Gly	Gly	275	280	285	
Ala	Pro	Trp	Gly	Met	Phe	Leu	Gly	Pro	Gln	Glu	Leu	Gln	His	Ile	Pro				

290 295 300

Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp Ser
 305 310 315 320

Lys Arg

<210> 17
 <211> 1650
 <212> DNA
 <213> Lycopersicon esculentum

<220>
 <221> CDS
 <222> (112)..(1614)

<400> 17

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aggaccccat ttgaagtttt cttgaaacaa atattaccct gttggaaaaa g atg gat 117
 Met Asp
 1

act ttg ttg aaa acc cca aat aac ctt gaa ttt ctg aac cca cat cat 165
 Thr Leu Leu Lys Thr Pro Asn Asn Leu Glu Phe Leu Asn Pro His His
 5 10 15

ggt ttt gct gtt aaa gct agt acc ttt aga tct gag aag cat cat aat 213
 Gly Phe Ala Val Lys Ala Ser Thr Phe Arg Ser Glu Lys His His Asn
 20 25 30

ttt ggt tct agg aag ttt tgt gaa act ttg ggt aga agt gtt tgt gtt 261
 Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val Cys Val
 35 40 45 50

aag ggt agt agt agt gct ctt tta gag ctt gta cct gag acc aaa aag 309
 Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr Lys Lys
 55 60 65

gag aat ctt gat ttt gag ctt cct atg tat gac cct tca aaa ggg gtt 357
 Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys Gly Val
 70 75 80

gtt gtg gat ctt gct gtg gtt ggt ggt ggc cct gca gga ctt gct gtt 405
 Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu Ala Val
 85 90 95

gca cag caa gtt tct gaa gca gga ctc tct gtt tgt tca att gat ccg 453
 Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile Asp Pro
 100 105 110

aat cct aaa ttg ata tgg cct aat aac tat ggt gtt tgg gtg gat gaa 501
 Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu
 115 120 125 130

ttt gag gct atg gac ttg tta gat tgt cta gat gct acc tgg tct ggt 549
 Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp Ser Gly

				135				140				145							
gca	gca	gtg	tac	att	gat	gat	aat	acg	gct	aaa	gat	ctt	cat	aga	cct		597		
Ala	Ala	Val	Tyr	Ile	Asp	Asp	Asn	Thr	Ala	Lys	Asp	Leu	His	Arg	Pro				
150								155				160							
tat	gga	agg	gtt	aac	cgg	aaa	cag	ctg	aaa	tcg	aaa	atg	atg	cag	aaa		645		
Tyr	Gly	Arg	Val	Asn	Arg	Lys	Gln	Leu	Lys	Ser	Lys	Met	Met	Gln	Lys				
165								170				175							
tgt	ata	atg	aat	ggt	gtt	aaa	ttc	cac	caa	gcc	aaa	gtt	ata	aag	gtg		693		
Cys	Ile	Met	Asn	Gly	Val	Lys	Phe	His	Gln	Ala	Lys	Val	Ile	Lys	Val				
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Ile	His	Glu	Glu	Ser	Lys	Ser	Met	Leu	Ile	Cys	Asn	Asp	Gly	Ile	Thr				
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Ile	Gln	Ala	Thr	Val	Val	Leu	Asp	Ala	Thr	Gly	Phe	Ser	Arg	Ser	Leu				
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Val	Gln	Tyr	Asp	Lys	Pro	Tyr	Asn	Pro	Gly	Tyr	Gln	Val	Ala	Tyr	Gly				
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Ile	Leu	Ala	Glu	Val	Glu	Glu	His	Pro	Phe	Asp	Val	Asn	Lys	Met	Val				
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Phe	Met	Asp	Trp	Arg	Asp	Ser	His	Leu	Lys	Asn	Asn	Thr	Asp	Leu	Lys				
260				265								270							
gag	aga	aat	agt	aga	ata	cca	act	ttt	ctt	tat	gca	atg	cca	ttt	tca		981		
Glu	Arg	Asn	Ser	Arg	Ile	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	Phe	Ser				
275				280								285				290			
tcc	aac	agg	ata	ttt	ctt	gaa	gaa	aca	tca	ctc	gta	gct	cgt	cct	ggc		1029		
Ser	Asn	Arg	Ile	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ala	Arg	Pro	Gly				
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Leu	Arg	Ile	Asp	Asp	Ile	Gln	Glu	Arg	Met	Val	Ala	Arg	Leu	Asn	His				
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Leu	Gly	Ile	Lys	Val	Lys	Ser	Ile	Glu	Glu	Asp	Glu	His	Cys	Leu	Ile				
325								330				335							
cca	atg	ggt	ggt	cca	ctt	cca	gta	tta	cct	cag	aga	gtc	gtt	gga	atc		1173		
Pro	Met	Gly	Gly	Pro	Leu	Pro	Val	Leu	Pro	Gln	Arg	Val	Val	Gly	Ile				
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Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile Gln Tyr
 375 380 385
 ctc ggt tct gaa aga agt cat tcg ggt aat gaa tta tcc aca gct gtt 1317
 Leu Gly Ser Glu Arg Ser His Ser Gly Asn Glu Leu Ser Thr Ala Val
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 Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu Phe Phe
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 tgc ttc ggt atg gat att ctt ctg aag ctt gat tta cct gct aca aga 1413
 Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala Thr Arg
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 Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp His Gly
 435 440 445 450
 ttc tta tcg tct cga ttg ttt cta cct gaa ctc ata gtt ttt ggg ctg 1509
 Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe Gly Leu
 455 460 465
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 Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile Met Thr
 470 475 480
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 Lys Gly Thr Val Pro Leu Val Asn Met Ile Asn Asn Leu Leu Gln Asp
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 Lys Glu
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<400> 18

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 His His Gly Phe Ala Val Lys Ala Ser Thr Phe Arg Ser Glu Lys His
 20 25 30
 His Asn Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val
 35 40 45
 Cys Val Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr
 50 55 60
 Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys
 65 70 75 80
 Gly Val Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu

85	90	95
Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile 100 105 110		
Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val 115 120 125		
Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp 130 135 140		
Ser Gly Ala Ala Val Tyr Ile Asp Asp Asn Thr Ala Lys Asp Leu His 145 150 155 160		
Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met 165 170 175		
Gln Lys Cys Ile Met Asn Gly Val Lys Phe His Gln Ala Lys Val Ile 180 185 190		
Lys Val Ile His Glu Glu Ser Lys Ser Met Leu Ile Cys Asn Asp Gly 195 200 205		
Ile Thr Ile Gln Ala Thr Val Val Leu Asp Ala Thr Gly Phe Ser Arg 210 215 220		
Ser Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala 225 230 235 240		
Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Val Asn Lys 245 250 255		
Met Val Phe Met Asp Trp Arg Asp Ser His Leu Lys Asn Asn Thr Asp 260 265 270		
Leu Lys Glu Arg Asn Ser Arg Ile Pro Thr Phe Leu Tyr Ala Met Pro 275 280 285		
Phe Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg 290 295 300		
Pro Gly Leu Arg Ile Asp Asp Ile Gln Glu Arg Met Val Ala Arg Leu 305 310 315 320		
Asn His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys 325 330 335		
Leu Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val 340 345 350		
Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met 355 360 365		
Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile 370 375 380		
Gln Tyr Leu Gly Ser Glu Arg Ser His Ser Gly Asn Glu Leu Ser Thr		

385 390 395 400

Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu
 405 410 415

Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala
 420 425 430

Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp
 435 440 445

His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe
 450 455 460

Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile
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Gln Asp Lys Glu
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 <212> DNA
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 <212> DNA
 <213> Nostoc sp. Strain PCC7120

<220>
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<400> 21

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ttatcttatt tttatgggca attagtttaa tcttattact ctcaatagat acatccataa    180
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attttatagg taagctcact ctaatcttgt atggactact cccttataaa gatttattga    360
aaaaacattg gttacaccac ggacatcctg gtactgattt agaccctgat tattacaatg    420
gtcatcccca aaacttcttt ctttggtatc tacattttat gaagtcttat tggcgatgga    480
cgcaaathtt cggattagtg atgatttttc atggacttaa aaatctggtg catataccag    540
aaaataatht aattatattt tggatgatac cttctatttt aagttcagta caactatttt    600
attttggtac atttttgcct cataaaaagc tagaagggtg ttatactaac cccattgtg    660
cgcgcgatgt cccattacct cttttttggt cttttgttac ttgttatcac ttcggctacc    720
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<212> DNA
<213> Unknown

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<220>
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<213> Unknown

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<220>

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<222> (3631)..(4158)

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agcggct	atg	caa	ccg	cat	tat	gat	ctg	att	ctc	gtg	ggg	gct	gga	ctc	169
	Met	Gln	Pro	His	Tyr	Asp	Leu	Ile	Leu	Val	Gly	Ala	Gly	Leu	
	1				5					10					

gcg	aat	ggc	ctt	atc	gcc	ctg	cgt	ctt	cag	cag	cag	caa	cct	gat	atg	217
Ala	Asn	Gly	Leu	Ile	Ala	Leu	Arg	Leu	Gln	Gln	Gln	Gln	Pro	Asp	Met	
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Arg	Ile	Leu	Leu	Ile	Asp	Ala	Ala	Pro	Gln	Ala	Gly	Gly	Asn	His	Thr	
				35				40						45		

tgg	tca	ttt	cac	cac	gat	gat	ttg	act	gag	agc	caa	cat	cgt	tgg	ata	313
Trp	Ser	Phe	His	His	Asp	Asp	Leu	Thr	Glu	Ser	Gln	His	Arg	Trp	Ile	
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gct	ccg	ctg	gtg	gtt	cat	cac	tgg	ccc	gac	tat	cag	gta	cgc	ttt	ccc	361
Ala	Pro	Leu	Val	Val	His	His	Trp	Pro	Asp	Tyr	Gln	Val	Arg	Phe	Pro	
		65					70					75				

aca	cgc	cgt	cgt	aag	ctg	aac	agc	ggc	tac	ttt	tgt	att	act	tct	cag	409
Thr	Arg	Arg	Arg	Lys	Leu	Asn	Ser	Gly	Tyr	Phe	Cys	Ile	Thr	Ser	Gln	
	80					85					90					

cgt	ttc	gct	gag	gtt	tta	cag	cga	cag	ttt	ggc	ccg	cac	ttg	tgg	atg	457
Arg	Phe	Ala	Glu	Val	Leu	Gln	Arg	Gln	Phe	Gly	Pro	His	Leu	Trp	Met	
95					100				105					110		

gat	acc	gcg	gtc	gca	gag	gtt	aat	gcg	gaa	tct	gtt	cgg	ttg	aaa	aag	505
Asp	Thr	Ala	Val	Ala	Glu	Val	Asn	Ala	Glu	Ser	Val	Arg	Leu	Lys	Lys	
				115				120						125		

ggt	cag	gtt	atc	ggt	gcc	cgc	gcg	gtg	att	gac	ggg	cgg	ggt	tat	gcg	553
Gly	Gln	Val	Ile	Gly	Ala	Arg	Ala	Val	Ile	Asp	Gly	Arg	Gly	Tyr	Ala	
			130					135					140			

gca	aat	tca	gca	ctg	agc	gtg	ggc	ttc	cag	gcg	ttt	att	ggc	cag	gaa	601
Ala	Asn	Ser	Ala	Leu	Ser	Val	Gly	Phe	Gln	Ala	Phe	Ile	Gly	Gln	Glu	
	145						150					155				

tgg	cga	ttg	agc	cac	ccg	cat	ggt	tta	tcg	tct	ccc	att	atc	atg	gat	649
Trp	Arg	Leu	Ser	His	Pro	His	Gly	Leu	Ser	Ser	Pro	Ile	Ile	Met	Asp	
	160					165					170					

gcc	acg	gtc	gat	cag	caa	aat	ggt	tat	cgc	ttc	gtg	tac	agc	ctg	ccg	697
Ala	Thr	Val	Asp	Gln	Gln	Asn	Gly	Tyr	Arg	Phe	Val	Tyr	Ser	Leu	Pro	
175					180				185					190		

ctc tcg ccg acc aga ttg tta att gaa gac acg cac tat att gat aat	745
Leu Ser Pro Thr Arg Leu Leu Ile Glu Asp Thr His Tyr Ile Asp Asn	
195 200 205	
gcg aca tta gat cct gaa tgc gcg cgg caa aat att tgc gac tat gcc	793
Ala Thr Leu Asp Pro Glu Cys Ala Arg Gln Asn Ile Cys Asp Tyr Ala	
210 215 220	
gcg caa cag ggt tgg cag ctt cag aca ctg ctg cga gaa gaa cag ggc	841
Ala Gln Gln Gly Trp Gln Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly	
225 230 235	
gcc tta ccc att act ctg tcg ggc aat gcc gac gca ttc tgg cag cag	889
Ala Leu Pro Ile Thr Leu Ser Gly Asn Ala Asp Ala Phe Trp Gln Gln	
240 245 250	
cgc ccc ctg gcc tgt agt gga tta cgt gcc ggt ctg ttc cat cct acc	937
Arg Pro Leu Ala Cys Ser Gly Leu Arg Ala Gly Leu Phe His Pro Thr	
255 260 265 270	
acc ggc tat tca ctg ccg ctg gcg gtt gcc gtg gcc gac cgc ctg agt	985
Thr Gly Tyr Ser Leu Pro Leu Ala Val Ala Val Ala Asp Arg Leu Ser	
275 280 285	
gca ctt gat gtc ttt acg tcg gcc tca att cac cat gcc att acg cat	1033
Ala Leu Asp Val Phe Thr Ser Ala Ser Ile His His Ala Ile Thr His	
290 295 300	
ttt gcc cgc gag cgc tgg cag cag cag ggc ttt ttc cgc atg ctg aat	1081
Phe Ala Arg Glu Arg Trp Gln Gln Gln Gly Phe Phe Arg Met Leu Asn	
305 310 315	
cgc atg ctg ttt tta gcc gga ccc gcc gat tca cgc tgg cgg gtt atg	1129
Arg Met Leu Phe Leu Ala Gly Pro Ala Asp Ser Arg Trp Arg Val Met	
320 325 330	
cag cgt ttt tat ggt tta cct gaa gat tta att gcc cgt ttt tat gcg	1177
Gln Arg Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala	
335 340 345 350	
gga aaa ctc acg ctg acc gat cgg cta cgt att ctg agc ggc aag ccg	1225
Gly Lys Leu Thr Leu Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro	
355 360 365	
cct gtt ccg gta tta gca gca ttg caa gcc att atg acg act	1267
Pro Val Pro Val Leu Ala Ala Leu Gln Ala Ile Met Thr Thr	
370 375 380	
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Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe	
385 390	
ggt ggc ctg gca ctg gca att cgt cta caa gct gcg ggg atc ccc gtc	1368
Gly Gly Leu Ala Leu Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val	
395 400 405	
tta ctg ctt gaa caa cgt gat aaa ccc ggc ggt cgg gct tat gtc tac	1416

Leu	Leu	Leu	Glu	Gln	Arg	Asp	Lys	Pro	Gly	Gly	Arg	Ala	Tyr	Val	Tyr	
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gag	gat	cag	ggg	ttt	acc	ttt	gat	gca	ggc	ccg	acg	gtt	atc	acc	gat	1464
Glu	Asp	Gln	Gly	Phe	Thr	Phe	Asp	Ala	Gly	Pro	Thr	Val	Ile	Thr	Asp	
	425						430				435					
ccc	agt	gcc	att	gaa	gaa	ctg	ttt	gca	ctg	gca	gga	aaa	cag	tta	aaa	1512
Pro	Ser	Ala	Ile	Glu	Glu	Leu	Phe	Ala	Leu	Ala	Gly	Lys	Gln	Leu	Lys	
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Glu	Tyr	Val	Glu	Leu	Leu	Pro	Val	Thr	Pro	Phe	Tyr	Arg	Leu	Cys	Trp	
			460						465					470		
gag	tca	ggg	aag	gtc	ttt	aat	tac	gat	aac	gat	caa	acc	cgg	ctc	gaa	1608
Glu	Ser	Gly	Lys	Val	Phe	Asn	Tyr	Asp	Asn	Asp	Gln	Thr	Arg	Leu	Glu	
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Ala	Gln	Ile	Gln	Gln	Phe	Asn	Pro	Arg	Asp	Val	Glu	Gly	Tyr	Arg	Gln	
	490						495					500				
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Phe	Leu	Asp	Tyr	Ser	Arg	Ala	Val	Phe	Lys	Glu	Gly	Tyr	Leu	Lys	Leu	
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Gly	Thr	Val	Pro	Phe	Leu	Ser	Phe	Arg	Asp	Met	Leu	Arg	Ala	Ala	Pro	
520					525					530					535	
caa	ctg	gcg	aaa	ctg	cag	gca	tgg	aga	agc	gtt	tac	agt	aag	gtt	gcc	1800
Gln	Leu	Ala	Lys	Leu	Gln	Ala	Trp	Arg	Ser	Val	Tyr	Ser	Lys	Val	Ala	
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agt	tac	atc	gaa	gat	gaa	cat	ctg	cgc	cag	gcg	ttt	tct	ttc	cac	tcg	1848
Ser	Tyr	Ile	Glu	Asp	Glu	His	Leu	Arg	Gln	Ala	Phe	Ser	Phe	His	Ser	
		555						560					565			
ctg	ttg	gtg	ggc	ggc	aat	ccc	ttc	gcc	acc	tca	tcc	att	tat	acg	ttg	1896
Leu	Leu	Val	Gly	Gly	Asn	Pro	Phe	Ala	Thr	Ser	Ser	Ile	Tyr	Thr	Leu	
		570				575							580			
ata	cac	gcg	ctg	gag	cgt	gag	tgg	ggc	gtc	tgg	ttt	ccg	cgt	ggc	ggc	1944
Ile	His	Ala	Leu	Glu	Arg	Glu	Trp	Gly	Val	Trp	Phe	Pro	Arg	Gly	Gly	
	585					590					595					
acc	ggc	gca	tta	gtt	cag	ggg	atg	ata	aag	ctg	ttt	cag	gat	ctg	ggc	1992
Thr	Gly	Ala	Leu	Val	Gln	Gly	Met	Ile	Lys	Leu	Phe	Gln	Asp	Leu	Gly	
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Gly	Glu	Val	Val	Leu	Asn	Ala	Arg	Val	Ser	His	Met	Glu	Thr	Thr	Gly	
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aac	aag	att	gaa	gcc	gtg	cat	tta	gag	gac	ggc	cgc	agg	ttc	ctg	acg	2088
Asn	Lys	Ile	Glu	Ala	Val	His	Leu	Glu	Asp	Gly	Arg	Arg	Phe	Leu	Thr	

635	640	645	
caa gcc gtc gcg tca aat gca gat gtg gtt cat acc tat cgc gac ctg Gln Ala Val Ala Ser Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu 650 655 660			2136
tta agc cag cac cct gcc gcg gtt aag cag tcc aac aaa ctg cag act Leu Ser Gln His Pro Ala Ala Val Lys Gln Ser Asn Lys Leu Gln Thr 665 670 675			2184
aag cgc atg agt aac tct ctg ttt gtg ctc tat ttt ggt ttg aat cac Lys Arg Met Ser Asn Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His 680 685 690 695			2232
cat cat gat cag ctc gcg cat cac acg gtt tgt ttc ggc ccg cgt tac His His Asp Gln Leu Ala His His Thr Val Cys Phe Gly Pro Arg Tyr 700 705 710			2280
cgc gag ctg att gac gaa att ttt aat cat gat ggc ctc gca gag gac Arg Glu Leu Ile Asp Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp 715 720 725			2328
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cct gaa ggt tgc ggc agt tac tat gtg ttg gcg ccg gtg ccg cat tta Pro Glu Gly Cys Gly Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu 745 750 755			2424
ggc acc gcg aac ctc gac tgg acg gtt gag ggg cca aaa cta cgc gac Gly Thr Ala Asn Leu Asp Trp Thr Val Glu Gly Pro Lys Leu Arg Asp 760 765 770 775			2472
cgt att ttt gcg tac ctt gag cag cat tac atg cct ggc tta cgg agt Arg Ile Phe Ala Tyr Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser 780 785 790			2520
cag ctg gtc acg cac cgg atg ttt acg ccg ttt gat ttt cgc gac cag Gln Leu Val Thr His Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Gln 795 800 805			2568
ctt aat gcc tat cat ggc tca gcc ttt tct gtg gag ccc gtt ctt acc Leu Asn Ala Tyr His Gly Ser Ala Phe Ser Val Glu Pro Val Leu Thr 810 815 820			2616
cag agc gcc tgg ttt cgg ccg cat aac cgc gat aaa acc att act aat Gln Ser Ala Trp Phe Arg Pro His Asn Arg Asp Lys Thr Ile Thr Asn 825 830 835			2664
ctc tac ctg gtc ggc gca ggc acg cat ccc ggc gca ggc att cct ggc Leu Tyr Leu Val Gly Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly 840 845 850 855			2712
gtc atc ggc tcg gca aaa gcg aca gca ggt ttg atg ctg gag gat ctg Val Ile Gly Ser Ala Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu 860 865 870			2760

att tga ataatccgtc gttactcaat catgcggtcg aaacg atg gca gtt ggc Ile	Met Ala Val Gly 875	2813
tcg aaa agt ttt gcg aca gcc tca aag tta ttt gat gca aaa acc cgg Ser Lys Ser Phe Ala Thr Ala Ser Lys Leu Phe Asp Ala Lys Thr Arg 880 885 890		2861
cgc agc gta ctg atg ctc tac gcc tgg tgc cgc cat tgt gac gat gtt Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His Cys Asp Asp Val 895 900 905		2909
att gac gat cag acg ctg gcc ttt cag gcc cgg cag cct gcc tta caa Ile Asp Asp Gln Thr Leu Gly Phe Gln Ala Arg Gln Pro Ala Leu Gln 910 915 920		2957
acg ccc gaa caa cgt ctg atg caa ctt gag atg aaa acg cgc cag gcc Thr Pro Glu Gln Arg Leu Met Gln Leu Glu Met Lys Thr Arg Gln Ala 925 930 935 940		3005
tat gca gga tcg cag atg cac gaa ccg gcg ttt gcg gct ttt cag gaa Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala Ala Phe Gln Glu 945 950 955		3053
gtg gct atg gct cat gat atc gcc ccg gct tac gcg ttt gat cat ctg Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala Phe Asp His Leu 960 965 970		3101
gaa gcc ttc gcc atg gat gta cgc gaa gcg caa tac agc caa ctg gat Glu Gly Phe Ala Met Asp Val Arg Glu Ala Gln Tyr Ser Gln Leu Asp 975 980 985		3149
gat acg ctg cgc tat tgc tat cac gtt gca gcc gtt gtc gcc ttg atg Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val Val Gly Leu Met 990 995 1000		3197
atg gcg caa atc atg gcc gtg cgg gat aac gcc acg ctg gac cgc Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr Leu Asp Arg 1005 1010 1015		3242
gcc tgt gac ctt ggg ctg gca ttt cag ttg acc aat att gct cgc Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile Ala Arg 1020 1025 1030		3287
gat att gtg gac gat gcg cat gcg gcc cgc tgt tat ctg ccg gca Asp Ile Val Asp Asp Ala His Ala Gly Arg Cys Tyr Leu Pro Ala 1035 1040 1045		3332
agc tgg ctg gag cat gaa ggt ctg aac aaa gag aat tat gcg gca Ser Trp Leu Glu His Glu Gly Leu Asn Lys Glu Asn Tyr Ala Ala 1050 1055 1060		3377
cct gaa aac cgt cag gcg ctg agc cgt atc gcc cgt cgt ttg gtg Pro Glu Asn Arg Gln Ala Leu Ser Arg Ile Ala Arg Arg Leu Val 1065 1070 1075		3422
cag gaa gca gaa cct tac tat ttg tct gcc aca gcc gcc ctg gca		3467

[illegible]

$\langle 210 \rangle$	25
$\langle 211 \rangle$	380

<212> PRT

<213> *Erwinia uredovora*

<400> 25

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Met Gln Pro His Tyr Asp Leu Ile Leu Val Gly Ala Gly Leu Ala Asn
1      5      10      15

Gly Leu Ile Ala Leu Arg Leu Gln Gln Gln Gln Pro Asp Met Arg Ile
      20      25      30

Leu Leu Ile Asp Ala Ala Pro Gln Ala Gly Gly Asn His Thr Trp Ser
      35      40      45

Phe His His Asp Asp Leu Thr Glu Ser Gln His Arg Trp Ile Ala Pro
      50      55      60

Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Thr Arg
65      70      75      80

Arg Arg Lys Leu Asn Ser Gly Tyr Phe Cys Ile Thr Ser Gln Arg Phe
      85      90      95

Ala Glu Val Leu Gln Arg Gln Phe Gly Pro His Leu Trp Met Asp Thr
      100     105     110

Ala Val Ala Glu Val Asn Ala Glu Ser Val Arg Leu Lys Lys Gly Gln
      115     120     125

Val Ile Gly Ala Arg Ala Val Ile Asp Gly Arg Gly Tyr Ala Ala Asn
130     135     140

Ser Ala Leu Ser Val Gly Phe Gln Ala Phe Ile Gly Gln Glu Trp Arg
145     150     155     160

Leu Ser His Pro His Gly Leu Ser Ser Pro Ile Ile Met Asp Ala Thr
      165     170     175

Val Asp Gln Gln Asn Gly Tyr Arg Phe Val Tyr Ser Leu Pro Leu Ser
      180     185     190

Pro Thr Arg Leu Leu Ile Glu Asp Thr His Tyr Ile Asp Asn Ala Thr
      195     200     205

Leu Asp Pro Glu Cys Ala Arg Gln Asn Ile Cys Asp Tyr Ala Ala Gln
      210     215     220

Gln Gly Trp Gln Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly Ala Leu
225     230     235     240

Pro Ile Thr Leu Ser Gly Asn Ala Asp Ala Phe Trp Gln Gln Arg Pro
      245     250     255

Leu Ala Cys Ser Gly Leu Arg Ala Gly Leu Phe His Pro Thr Thr Gly
      260     265     270

Tyr Ser Leu Pro Leu Ala Val Ala Val Ala Asp Arg Leu Ser Ala Leu
      275     280     285

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Asp Val Phe Thr Ser Ala Ser Ile His His Ala Ile Thr His Phe Ala
 290 295 300
 Arg Glu Arg Trp Gln Gln Gln Gly Phe Phe Arg Met Leu Asn Arg Met
 305 310 315 320
 Leu Phe Leu Ala Gly Pro Ala Asp Ser Arg Trp Arg Val Met Gln Arg
 325 330 335
 Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala Gly Lys
 340 345 350
 Leu Thr Leu Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro Pro Val
 355 360 365
 Pro Val Leu Ala Ala Leu Gln Ala Ile Met Thr Thr
 370 375 380

<210> 26
 <211> 492
 <212> PRT
 <213> Erwinia uredovora

<400> 26

Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe Gly Gly Leu Ala Leu
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 Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln
 20 25 30
 Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Glu Asp Gln Gly Phe
 35 40 45
 Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu
 50 55 60
 Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Glu Tyr Val Glu Leu
 65 70 75 80
 Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val
 85 90 95
 Phe Asn Tyr Asp Asn Asp Gln Thr Arg Leu Glu Ala Gln Ile Gln Gln
 100 105 110
 Phe Asn Pro Arg Asp Val Glu Gly Tyr Arg Gln Phe Leu Asp Tyr Ser
 115 120 125
 Arg Ala Val Phe Lys Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe
 130 135 140
 Leu Ser Phe Arg Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu
 145 150 155 160
 Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Ser Tyr Ile Glu Asp
 165 170 175
 Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly

180	185	190
Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu		
195	200	205
Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val		
210	215	220
Gln Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu		
225	230	235
Asn Ala Arg Val Ser His Met Glu Thr Thr Gly Asn Lys Ile Glu Ala		
245	250	255
Val His Leu Glu Asp Gly Arg Arg Phe Leu Thr Gln Ala Val Ala Ser		
260	265	270
Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro		
275	280	285
Ala Ala Val Lys Gln Ser Asn Lys Leu Gln Thr Lys Arg Met Ser Asn		
290	295	300
Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu		
305	310	315
Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile Asp		
325	330	335
Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu		
340	345	350
His Ala Pro Cys Val Thr Asp Ser Ser Leu Ala Pro Glu Gly Cys Gly		
355	360	365
Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu		
370	375	380
Asp Trp Thr Val Glu Gly Pro Lys Leu Arg Asp Arg Ile Phe Ala Tyr		
385	390	395
Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His		
405	410	415
Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Gln Leu Asn Ala Tyr His		
420	425	430
Gly Ser Ala Phe Ser Val Glu Pro Val Leu Thr Gln Ser Ala Trp Phe		
435	440	445
Arg Pro His Asn Arg Asp Lys Thr Ile Thr Asn Leu Tyr Leu Val Gly		
450	455	460
Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala		
465	470	475
Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile		
485	490	

<210> 27
 <211> 296
 <212> PRT
 <213> Erwinia uredovora

<400> 27

Met	Ala	Val	Gly	Ser	Lys	Ser	Phe	Ala	Thr	Ala	Ser	Lys	Leu	Phe	Asp	1	5	10	15
Ala	Lys	Thr	Arg	Arg	Ser	Val	Leu	Met	Leu	Tyr	Ala	Trp	Cys	Arg	His	20	25	30	
Cys	Asp	Asp	Val	Ile	Asp	Asp	Gln	Thr	Leu	Gly	Phe	Gln	Ala	Arg	Gln	35	40	45	
Pro	Ala	Leu	Gln	Thr	Pro	Glu	Gln	Arg	Leu	Met	Gln	Leu	Glu	Met	Lys	50	55	60	
Thr	Arg	Gln	Ala	Tyr	Ala	Gly	Ser	Gln	Met	His	Glu	Pro	Ala	Phe	Ala	65	70	75	80
Ala	Phe	Gln	Glu	Val	Ala	Met	Ala	His	Asp	Ile	Ala	Pro	Ala	Tyr	Ala	85	90	95	
Phe	Asp	His	Leu	Glu	Gly	Phe	Ala	Met	Asp	Val	Arg	Glu	Ala	Gln	Tyr	100	105	110	
Ser	Gln	Leu	Asp	Asp	Thr	Leu	Arg	Tyr	Cys	Tyr	His	Val	Ala	Gly	Val	115	120	125	
Val	Gly	Leu	Met	Met	Ala	Gln	Ile	Met	Gly	Val	Arg	Asp	Asn	Ala	Thr	130	135	140	
Leu	Asp	Arg	Ala	Cys	Asp	Leu	Gly	Leu	Ala	Phe	Gln	Leu	Thr	Asn	Ile	145	150	155	160
Ala	Arg	Asp	Ile	Val	Asp	Asp	Ala	His	Ala	Gly	Arg	Cys	Tyr	Leu	Pro	165	170	175	
Ala	Ser	Trp	Leu	Glu	His	Glu	Gly	Leu	Asn	Lys	Glu	Asn	Tyr	Ala	Ala	180	185	190	
Pro	Glu	Asn	Arg	Gln	Ala	Leu	Ser	Arg	Ile	Ala	Arg	Arg	Leu	Val	Gln	195	200	205	
Glu	Ala	Glu	Pro	Tyr	Tyr	Leu	Ser	Ala	Thr	Ala	Gly	Leu	Ala	Gly	Leu	210	215	220	
Pro	Leu	Arg	Ser	Ala	Trp	Ala	Ile	Ala	Thr	Ala	Lys	Gln	Val	Tyr	Arg	225	230	235	240
Lys	Ile	Gly	Val	Lys	Val	Glu	Gln	Ala	Gly	Gln	Gln	Ala	Trp	Asp	Gln	245	250	255	
Arg	Gln	Ser	Thr	Thr	Thr	Pro	Glu	Lys	Leu	Thr	Leu	Leu	Leu	Ala	Ala	260	265	270	

Ser Gly Gln Ala Leu Thr Ser Arg Met Arg Ala His Pro Pro Arg Pro
 275 280 285

Ala His Leu Trp Gln Arg Pro Leu
 290 295

<210> 28
 <211> 32
 <212> DNA
 <213> Unknown

<220>
 <221> primer_bind
 <223> Artificial sequence

<400> 28
 tttttctcga gcgataaacg ctcacttggt ta 32

<210> 29
 <211> 32
 <212> DNA
 <213> Unknown

<220>
 <221> primer_bind
 <223> Artificial sequence

<400> 29
 tttttgtcga cacggttatgc tcacaacccc gg 32

<210> 30
 <211> 679
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (87)..(635)

<400> 30
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gtgatcagaa ttacatgtga gaaatt atg caa acg gaa cac gtc att tta ttg 113
 Met Gln Thr Glu His Val Ile Leu Leu
 1 5

aat gca cag gga gtt ccc acg ggt acg ctg gaa aag tat gcc gca cac 161
 Asn Ala Gln Gly Val Pro Thr Gly Thr Leu Glu Lys Tyr Ala Ala His
 10 15 20 25

acg gca gac acc cgc tta cat ctc gcg ttc tcc agt tgg ctg ttt aat 209
 Thr Ala Asp Thr Arg Leu His Leu Ala Phe Ser Ser Trp Leu Phe Asn
 30 35 40

gcc aaa gga caa tta tta gtt acc cgc cgc gca ctg agc aaa aaa gca 257

Ala Lys Gly Gln Leu Leu Val Thr Arg Arg Ala Leu Ser Lys Lys Ala	
45 50 55	
tgg cct ggc gtg tgg act aac tcg gtt tgt ggg cac cca caa ctg gga	305
Trp Pro Gly Val Trp Thr Asn Ser Val Cys Gly His Pro Gln Leu Gly	
60 65 70	
gaa agc aac gaa gac gca gtg atc cgc cgt tgc cgt tat gag ctt ggc	353
Glu Ser Asn Glu Asp Ala Val Ile Arg Arg Cys Arg Tyr Glu Leu Gly	
75 80 85	
gtg gaa att acg cct cct gaa tct atc tat cct gac ttt cgc tac cgc	401
Val Glu Ile Thr Pro Pro Glu Ser Ile Tyr Pro Asp Phe Arg Tyr Arg	
90 95 100 105	
gcc acc gat ccg agt ggc att gtg gaa aat gaa gtg tgt ccg gta ttt	449
Ala Thr Asp Pro Ser Gly Ile Val Glu Asn Glu Val Cys Pro Val Phe	
110 115 120	
gcc gca cgc acc act agt gcg tta cag atc aat gat gat gaa gtg atg	497
Ala Ala Arg Thr Thr Ser Ala Leu Gln Ile Asn Asp Asp Glu Val Met	
125 130 135	
gat tat caa tgg tgt gat tta gca gat gta tta cac ggt att gat gcc	545
Asp Tyr Gln Trp Cys Asp Leu Ala Asp Val Leu His Gly Ile Asp Ala	
140 145 150	
acg ccg tgg gcg ttc agt ccg tgg atg gtg atg cag gcg aca aat cgc	593
Thr Pro Trp Ala Phe Ser Pro Trp Met Val Met Gln Ala Thr Asn Arg	
155 160 165	
gaa gcc aga aaa cga tta tct gca ttt acc cag ctt aaa taa	635
Glu Ala Arg Lys Arg Leu Ser Ala Phe Thr Gln Leu Lys	
170 175 180	
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<210> 31	
<211> 182	
<212> PRT	
<213> Escherichia coli	
<400> 31	
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20 25 30	
Leu Ala Phe Ser Ser Trp Leu Phe Asn Ala Lys Gly Gln Leu Leu Val	
35 40 45	
Thr Arg Arg Ala Leu Ser Lys Lys Ala Trp Pro Gly Val Trp Thr Asn	
50 55 60	
Ser Val Cys Gly His Pro Gln Leu Gly Glu Ser Asn Glu Asp Ala Val	
65 70 75 80	

Ile Arg Arg Cys Arg Tyr Glu Leu Gly Val Glu Ile Thr Pro Pro Glu
 85 90 95
 Ser Ile Tyr Pro Asp Phe Arg Tyr Arg Ala Thr Asp Pro Ser Gly Ile
 100 105 110
 Val Glu Asn Glu Val Cys Pro Val Phe Ala Ala Arg Thr Thr Ser Ala
 115 120 125
 Leu Gln Ile Asn Asp Asp Glu Val Met Asp Tyr Gln Trp Cys Asp Leu
 130 135 140
 Ala Asp Val Leu His Gly Ile Asp Ala Thr Pro Trp Ala Phe Ser Pro
 145 150 155 160
 Trp Met Val Met Gln Ala Thr Asn Arg Glu Ala Arg Lys Arg Leu Ser
 165 170 175
 Ala Phe Thr Gln Leu Lys
 180

<210> 32
 <211> 31
 <212> DNA
 <213> Unknown

<220>
 <221> primer_bind
 <223> Artificial sequence

<400> 32
 tttttccatg gtgaaggagg aaatagcgaa a

31

<210> 33
 <211> 32
 <212> DNA
 <213> Unknown

<220>
 <221> primer_bind
 <223> Artificial sequence

<400> 33
 tttttaagct ttcacttttt tcttgtaacc aa

32

<210> 34
 <211> 962
 <212> DNA
 <213> Archaeoglobus fulgidus

<220>
 <221> CDS
 <222> (3)..(956)

<400> 34

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gcc att gaa gag ctt ctg ccc gaa agg gag ccg att gga ctc tac aaa Ala Ile Glu Glu Leu Leu Pro Glu Arg Glu Pro Ile Gly Leu Tyr Lys 20 25 30	95
gcc gca agg cat ctg atc aaa gca ggt ggc aag agg cta agg cct gta Ala Ala Arg His Leu Ile Lys Ala Gly Gly Lys Arg Leu Arg Pro Val 35 40 45	143
ata agc ctc tta gca gtc gaa gcc ctt ggg aaa gac tac aga aag att Ile Ser Leu Leu Ala Val Glu Ala Leu Gly Lys Asp Tyr Arg Lys Ile 50 55 60	191
atc ccg gct gct gtc agc att gaa aca atc cac aac ttc acc ctc gtg Ile Pro Ala Ala Val Ser Ile Glu Thr Ile His Asn Phe Thr Leu Val 65 70 75	239
cat gac gac ata atg gac agg gac gag atg agg agg gga gtt ccg acg His Asp Asp Ile Met Asp Arg Asp Glu Met Arg Arg Gly Val Pro Thr 80 85 90 95	287
gta cac agg gtt tat ggg gaa gcg acg gcc att tta gca ggc gac aca Val His Arg Val Tyr Gly Glu Ala Thr Ala Ile Leu Ala Gly Asp Thr 100 105 110	335
ctc ttt gct gaa gcc ttc aag ctg ctg aca aag tgc gat gtt gag agc Leu Phe Ala Glu Ala Phe Lys Leu Leu Thr Lys Cys Asp Val Glu Ser 115 120 125	383
gag gga atc aga aaa gct aca gaa atg ctt tcg gac gtt tgc ata aaa Glu Gly Ile Arg Lys Ala Thr Glu Met Leu Ser Asp Val Cys Ile Lys 130 135 140	431
ata tgc gag ggg cag tac tac gac atg agc ttt gag aaa aag gag agc Ile Cys Glu Gly Gln Tyr Tyr Asp Met Ser Phe Glu Lys Lys Glu Ser 145 150 155	479
gtt tcc gag gag gag tat ctc agg atg gtc gag ctg aag acc gga gtg Val Ser Glu Glu Glu Tyr Leu Arg Met Val Glu Leu Lys Thr Gly Val 160 165 170 175	527
ctg att gca gct tct gca gca tta cct gcg gtg ctt ttt ggg gag agc Leu Ile Ala Ala Ser Ala Ala Leu Pro Ala Val Leu Phe Gly Glu Ser 180 185 190	575
gag gaa att gta aag gcg ctg tgg gac tac gga gtt ctt agc ggt att Glu Glu Ile Val Lys Ala Leu Trp Asp Tyr Gly Val Leu Ser Gly Ile 195 200 205	623
ggc ttc cag atc cag gac gac ctg ctt gac ctg act gag gag acc gga Gly Phe Gln Ile Gln Asp Asp Leu Leu Asp Leu Thr Glu Glu Thr Gly 210 215 220	671
aag gac tgg gga agc gac ctg ctt aaa ggg aag aaa acc ctg att gtc Lys Asp Trp Gly Ser Asp Leu Leu Lys Gly Lys Lys Thr Leu Ile Val	719

Gly Ile Arg Lys Ala Thr Glu Met Leu Ser Asp Val Cys Ile Lys Ile
130 135 140

Cys Glu Gly Gln Tyr Tyr Asp Met Ser Phe Glu Lys Lys Glu Ser Val
 145 150 155 160
 Ser Glu Glu Glu Tyr Leu Arg Met Val Glu Leu Lys Thr Gly Val Leu
 165 170 175
 Ile Ala Ala Ser Ala Ala Leu Pro Ala Val Leu Phe Gly Glu Ser Glu
 180 185 190
 Glu Ile Val Lys Ala Leu Trp Asp Tyr Gly Val Leu Ser Gly Ile Gly
 195 200 205
 Phe Gln Ile Gln Asp Asp Leu Leu Asp Leu Thr Glu Glu Thr Gly Lys
 210 215 220
 Asp Trp Gly Ser Asp Leu Leu Lys Gly Lys Lys Thr Leu Ile Val Ile
 225 230 235 240
 Lys Ala Phe Glu Lys Gly Val Lys Leu Lys Thr Phe Gly Lys Glu Lys
 245 250 255
 Ala Asp Val Ser Glu Ile Arg Asp Asp Ile Glu Lys Leu Arg Glu Cys
 260 265 270
 Gly Ala Ile Asp Tyr Ala Ala Ser Met Ala Arg Lys Met Ala Glu Glu
 275 280 285
 Ala Lys Arg Lys Leu Glu Val Leu Pro Glu Ser Lys Ala Lys Glu Thr
 290 295 300
 Leu Leu Glu Leu Thr Asp Phe Leu Val Thr Arg Lys Lys
 305 310 315

<210> 36
 <211> 1293
 <212> DNA
 <213> *Archaeoglobus fulgidus*

<220>
 <221> CDS
 <222> (206)..(1159)

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 gggggcaggg atggctatat ttctgggagc gaactccggg cgaggatcta gttgtaggga 180
 gggattcatg acaccacaaa cagcc atg gtg aag gag gaa ata gcg aaa agg 232
 Met Val Lys Glu Glu Ile Ala Lys Arg
 1 5
 gcc gaa ata atc aac aaa gcc att gaa gag ctt ctg ccc gaa agg gag 280
 Ala Glu Ile Ile Asn Lys Ala Ile Glu Glu Leu Leu Pro Glu Arg Glu
 10 15 20 25

ccg att gga ctc tac aaa gcc gca agg cat ctg atc aaa gca ggt ggc	328
Pro Ile Gly Leu Tyr Lys Ala Ala Arg His Leu Ile Lys Ala Gly Gly	
30 35 40	
aag agg cta agg cct gta ata agc ctc tta gca gtc gaa gcc ctt ggg	376
Lys Arg Leu Arg Pro Val Ile Ser Leu Leu Ala Val Glu Ala Leu Gly	
45 50 55	
aaa gac tac aga aag att atc ccg gct gct gtc agc att gaa aca atc	424
Lys Asp Tyr Arg Lys Ile Ile Pro Ala Ala Val Ser Ile Glu Thr Ile	
60 65 70	
cac aac ttc acc ctc gtg cat gac gac ata atg gac agg gac gag atg	472
His Asn Phe Thr Leu Val His Asp Asp Ile Met Asp Arg Asp Glu Met	
75 80 85	
agg agg gga gtt ccg acg gta cac agg gtt tat ggg gaa gcg acg gcc	520
Arg Arg Gly Val Pro Thr Val His Arg Val Tyr Gly Glu Ala Thr Ala	
90 95 100 105	
att tta gca ggc gac aca ctc ttt gct gaa gcc ttc aag ctg ctg aca	568
Ile Leu Ala Gly Asp Thr Leu Phe Ala Glu Ala Phe Lys Leu Leu Thr	
110 115 120	
aag tgc gat gtt gag agc gag gga atc aga aaa gct aca gaa atg ctt	616
Lys Cys Asp Val Glu Ser Glu Gly Ile Arg Lys Ala Thr Glu Met Leu	
125 130 135	
tcg gac gtt tgc ata aaa ata tgc gag ggg cag tac tac gac atg agc	664
Ser Asp Val Cys Ile Lys Ile Cys Glu Gly Gln Tyr Tyr Asp Met Ser	
140 145 150	
ttt gag aaa aag gag agc gtt tcc gag gag gag tat ctc agg atg gtc	712
Phe Glu Lys Lys Glu Ser Val Ser Glu Glu Glu Tyr Leu Arg Met Val	
155 160 165	
gag ctg aag acc gga gtg ctg att gca gct tct gca gca tta cct gcg	760
Glu Leu Lys Thr Gly Val Leu Ile Ala Ala Ser Ala Ala Leu Pro Ala	
170 175 180 185	
gtg ctt ttt ggg gag agc gag gaa att gta aag gcg ctg tgg gac tac	808
Val Leu Phe Gly Glu Ser Glu Glu Ile Val Lys Ala Leu Trp Asp Tyr	
190 195 200	
gga gtt ctt agc ggt att ggc ttc cag atc cag gac gac ctg ctt gac	856
Gly Val Leu Ser Gly Ile Gly Phe Gln Ile Gln Asp Asp Leu Leu Asp	
205 210 215	
ctg act gag gag acc gga aag gac tgg gga agc gac ctg ctt aaa ggg	904
Leu Thr Glu Glu Thr Gly Lys Asp Trp Gly Ser Asp Leu Leu Lys Gly	
220 225 230	
aag aaa acc ctg att gtc ata aag gcg ttc gaa aag gga gtg aag cta	952
Lys Lys Thr Leu Ile Val Ile Lys Ala Phe Glu Lys Gly Val Lys Leu	
235 240 245	
aag acg ttt gga aag gaa aag gcg gac gtc tct gag att aga gat gat	1000

Lys Thr Phe Gly Lys Glu Lys Ala Asp Val Ser Glu Ile Arg Asp Asp
 250 255 260 265
 atc gaa aag tta aga gag tgt ggt gcg att gat tac gct gcc agc atg 1048
 Ile Glu Lys Leu Arg Glu Cys Gly Ala Ile Asp Tyr Ala Ala Ser Met
 270 275 280
 gca aga aag atg gct gaa gag gcg aaa aga aag ctc gaa gtt ctg cct 1096
 Ala Arg Lys Met Ala Glu Glu Ala Lys Arg Lys Leu Glu Val Leu Pro
 285 290 295
 gaa agc aaa gcc aag gaa aca ctg ctg gaa ctt acc gac ttc ttg gtt 1144
 Glu Ser Lys Ala Lys Glu Thr Leu Leu Glu Leu Thr Asp Phe Leu Val
 300 305 310
 aca aga aaa aag tga aagcttcaat tgcattgctct agatgatcaa agaattcctg 1199
 Thr Arg Lys Lys
 315
 gcctagtcta taggagggttt tgaaaagaaa ggagcaataa tcattttctt gttctatcaa 1259
 gaggggtgcta ttgctccttt ctttttttct cgag 1293

 <210> 37
 <211> 317
 <212> PRT
 <213> Archaeoglobus fulgidus

 <400> 37

 Met Val Lys Glu Glu Ile Ala Lys Arg Ala Glu Ile Ile Asn Lys Ala
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 20 25 30
 Ala Arg His Leu Ile Lys Ala Gly Gly Lys Arg Leu Arg Pro Val Ile
 35 40 45
 Ser Leu Leu Ala Val Glu Ala Leu Gly Lys Asp Tyr Arg Lys Ile Ile
 50 55 60
 Pro Ala Ala Val Ser Ile Glu Thr Ile His Asn Phe Thr Leu Val His
 65 70 75 80
 Asp Asp Ile Met Asp Arg Asp Glu Met Arg Arg Gly Val Pro Thr Val
 85 90 95
 His Arg Val Tyr Gly Glu Ala Thr Ala Ile Leu Ala Gly Asp Thr Leu
 100 105 110
 Phe Ala Glu Ala Phe Lys Leu Leu Thr Lys Cys Asp Val Glu Ser Glu
 115 120 125
 Gly Ile Arg Lys Ala Thr Glu Met Leu Ser Asp Val Cys Ile Lys Ile
 130 135 140
 Cys Glu Gly Gln Tyr Tyr Asp Met Ser Phe Glu Lys Lys Glu Ser Val

145 150 155 160
 Ser Glu Glu Glu Tyr Leu Arg Met Val Glu Leu Lys Thr Gly Val Leu
 165 170 175
 Ile Ala Ala Ser Ala Ala Leu Pro Ala Val Leu Phe Gly Glu Ser Glu
 180 185 190
 Glu Ile Val Lys Ala Leu Trp Asp Tyr Gly Val Leu Ser Gly Ile Gly
 195 200 205
 Phe Gln Ile Gln Asp Asp Leu Leu Asp Leu Thr Glu Glu Thr Gly Lys
 210 215 220
 Asp Trp Gly Ser Asp Leu Leu Lys Gly Lys Lys Thr Leu Ile Val Ile
 225 230 235 240
 Lys Ala Phe Glu Lys Gly Val Lys Leu Lys Thr Phe Gly Lys Glu Lys
 245 250 255
 Ala Asp Val Ser Glu Ile Arg Asp Asp Ile Glu Lys Leu Arg Glu Cys
 260 265 270
 Gly Ala Ile Asp Tyr Ala Ala Ser Met Ala Arg Lys Met Ala Glu Glu
 275 280 285
 Ala Lys Arg Lys Leu Glu Val Leu Pro Glu Ser Lys Ala Lys Glu Thr
 290 295 300
 Leu Leu Glu Leu Thr Asp Phe Leu Val Thr Arg Lys Lys
 305 310 315

<210> 38
 <211> 35
 <212> DNA
 <213> Unknown

<220>
 <221> primer_bind
 <223> Artificial sequence

<400> 38
 gagctcttca ttatttcgat tttgatttcg tgacc

35

<210> 39
 <211> 38
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer

<400> 39
 aagcttggtt gatcagaaga agaagaagaa gatgaact

38

<210> 40

<211> 647
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> Promoter

<400> 40
 gagctcttca ttatttcgat tttgatttcg tgaccagcga acgcagaata ccttggtgtg 60
 taatacttta cccgtgtaaa tcaaaaacaa aaaggctttt gagctttttg tagttgaatt 120
 tctctggctg atcttttctg tacagattca tatatctgca gagacgatat cattgattat 180
 ttgagcttct tttgaactat ttcgtgtaat ttgggatgag agctctatgt atgtgtgtaa 240
 actttgaaga caacaagaaa ggtaacaagt gagggagggg tgactccatg tcaaaataga 300
 tgtcataaga ggcccatcaa taagtgtttg agcccattag ctagcccagt aactaccaga 360
 ttgtgagatg gatgtgtgaa cagttttttt ttgatgtag gactgaaatg tgaacaacag 420
 gcgcatgaaa ggctaaatta ggacaatgat aagcagaaat aacttatcct ctctaact 480
 tggcctcaca ttgcccttca cacaatccac acacatccaa tcacaacctc atcatatc 540
 tcccgcta atcttttttct ttgatctttt tttttttgct tattattttt ttgactttga 600
 tctcccatca gttcatcttc ttcttcttct tctgatcaac caagctt 647

<210> 41
 <211> 28
 <212> DNA
 <213> Unknown

<220>
 <221> primer_bind
 <223> Artificial sequence

<400> 41
 gagctcactc actgatttcc attgcttg 28

<210> 42
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer

<400> 42
 aagcttttgt tgaagagatt tgg 23

<210> 43
 <211> 37
 <212> DNA
 <213> Unknown

<220>
 <221> primer_bind
 <223> Artificial sequence

<400> 43
 cgccgttaag tcgatgtccg ttgatttaaa cagtgtc 37

<210> 44
 <211> 34
 <212> DNA
 <213> Unknown

<220>
 <221> primer_bind
 <223> Artificial sequence

<400> 44
 atcaacggac atcgacttaa cggcgtttgt aaac 34

<210> 45
 <211> 777
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> Promoter

<400> 45
 gagctcactc actgatttcc attgcttgaa aattgatgat gaactaagat caatccatgt 60
 tagtttcaaa acaacagtaa ctgtggccaa cttagttttg aaacaacact aactggtcga 120
 agcaaaaaga aaaaagagtt tcatcatata tctgatttga tggactgttt ggagtttagga 180
 ccaaacatta tctacaaaca aagacttttc tcttaacttg tgattccttc ttaaacccta 240
 ggggtaatat tctattttcc aaggatcttt agttaaaggc aaatccggga aattattgta 300
 atcatttggg gaaacatata aaagatttga gttagatgga agtgacgatt aatccaaaca 360
 tatatatctc tttcttctta tttcccaaataaacagacaa aagtagaata ttggctttta 420
 acaccaatat aaaaacttgc ttcacaccta aacacttttg tttacttttag ggtaagtgca 480
 aaaagccaac caaatccacc tgcactgatt tgacgtttac aaacgccgtt aagtcgatgt 540
 ccgttgattt aaacagtgtc ttgtaattaa aaaaatcagt ttacataaat ggaaaattta 600
 tcacttagtt ttcataact tctgaactta cctttcatgg attaggcaat actttccatt 660
 ttttagtaact caagtggacc ctttacttct tcaactccat ctctctcttt ctatttcaact 720
 tctttcttct cattatatct cttgtcctct ccaccaaatac tcttcaacaa aaagctt 777

<210> 46
 <211> 804
 <212> DNA
 <213> Synechococcus WH8102

<220>
 <221> CDS

<400> 46
 atg aaa acg aca aga tct att tcg tgg cca tcg act tgc tgg cat cac 48
 Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His
 1 5 10 15
 cag ccg agt tgc tca agc tgg gtg gca aat gag ttc agc cct cag gcc 96
 Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala
 20 25 30
 ctc aaa ggg ttg gct ctg gct ggt ctg att gga tca gcc tgg ctg ctc 144
 Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu
 35 40 45

tcc ctg ggc ctg agc tac acc ctg cca ctt gat cag acg cct ggg ctg Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu 50 55 60	192
ttg att ggc agc ttg att ctg ctc aga gca ttt ctg cac acc ggg ctg Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu 65 70 75 80	240
ttc atc gtt gcc cac gat tcc atg cac gcc agt ctg gtt ccg ggt cat Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His 85 90 95	288
ccc gga ttg aac cgc tgg atc ggc aaa gtg tat ttg ttg gtg tat gca Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala 100 105 110	336
ggc ttg tct tat gag cgt tgt tcc cgc aac cac aga cgt cat cac ctg Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu 115 120 125	384
gca ccg gag acg ttc cag gat cct gac tac caa cgt tgc acc aat aac Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn 130 135 140	432
aac atc cta gat tgg tat gtt cac ttc atg ggc aac tat ctg ggc atg Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met 145 150 155 160	480
cgg caa ctg tta aat cta agc tgt ctt tgg ctg gcg cta atc att ctc Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu 165 170 175	528
aac ggt tct gat ctc cct gct cag atc atg cat ctg ctg ttg ttc agc Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser 180 185 190	576
gtt ctg ccg ttg atc atc agt tcc tgt caa ttg ttt cta gtg gga acc Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr 195 200 205	624
tgg tta ccc cac cga cgt ggg gcc acg aca cga ccg ggc gtg aca acg Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr 210 215 220	672
cgc agc ctg gct ttg cat cca gcc ctc tct ttc gca gct tgt tac aac Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn 225 230 235 240	720
ttt ggc tat cat cgt gaa cat cat gaa tcg cct tcc aca ccc tgg ttt Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe 245 250 255	768
cag ctg cca caa ctt cga aat gaa tca ttc act tga Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr 260 265	804

<210> 47
 <211> 267
 <212> PRT
 <213> Synechococcus WH8102

<400> 47

Met	Lys	Thr	Thr	Arg	Ser	Ile	Ser	Trp	Pro	Ser	Thr	Cys	Trp	His	His	1	5	10	15
Gln	Pro	Ser	Cys	Ser	Ser	Trp	Val	Ala	Asn	Glu	Phe	Ser	Pro	Gln	Ala	20	25	30	
Leu	Lys	Gly	Leu	Ala	Leu	Ala	Gly	Leu	Ile	Gly	Ser	Ala	Trp	Leu	Leu	35	40	45	
Ser	Leu	Gly	Leu	Ser	Tyr	Thr	Leu	Pro	Leu	Asp	Gln	Thr	Pro	Gly	Leu	50	55	60	
Leu	Ile	Gly	Ser	Leu	Ile	Leu	Leu	Arg	Ala	Phe	Leu	His	Thr	Gly	Leu	65	70	75	80
Phe	Ile	Val	Ala	His	Asp	Ser	Met	His	Ala	Ser	Leu	Val	Pro	Gly	His	85	90	95	
Pro	Gly	Leu	Asn	Arg	Trp	Ile	Gly	Lys	Val	Tyr	Leu	Leu	Val	Tyr	Ala	100	105	110	
Gly	Leu	Ser	Tyr	Glu	Arg	Cys	Ser	Arg	Asn	His	Arg	Arg	His	His	Leu	115	120	125	
Ala	Pro	Glu	Thr	Phe	Gln	Asp	Pro	Asp	Tyr	Gln	Arg	Cys	Thr	Asn	Asn	130	135	140	
Asn	Ile	Leu	Asp	Trp	Tyr	Val	His	Phe	Met	Gly	Asn	Tyr	Leu	Gly	Met	145	150	155	160
Arg	Gln	Leu	Leu	Asn	Leu	Ser	Cys	Leu	Trp	Leu	Ala	Leu	Ile	Ile	Leu	165	170	175	
Asn	Gly	Ser	Asp	Leu	Pro	Ala	Gln	Ile	Met	His	Leu	Leu	Leu	Phe	Ser	180	185	190	
Val	Leu	Pro	Leu	Ile	Ile	Ser	Ser	Cys	Gln	Leu	Phe	Leu	Val	Gly	Thr	195	200	205	
Trp	Leu	Pro	His	Arg	Arg	Gly	Ala	Thr	Thr	Arg	Pro	Gly	Val	Thr	Thr	210	215	220	
Arg	Ser	Leu	Ala	Leu	His	Pro	Ala	Leu	Ser	Phe	Ala	Ala	Cys	Tyr	Asn	225	230	235	240
Phe	Gly	Tyr	His	Arg	Glu	His	His	Glu	Ser	Pro	Ser	Thr	Pro	Trp	Phe	245	250	255	
Gln	Leu	Pro	Gln	Leu	Arg	Asn	Glu	Ser	Phe	Thr						260	265		

<210> 48
 <211> 804
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <223> Artificial variant

<400> 48
 atg aaa acg aca aga tct att tcg tgg cca tcg act tgc tgg cat cac 48
 Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His
 1 5 10 15

cag ccg agt tgc tca agc tgg gtg gca aat gag ttc agc cct cag gcc 96
 Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala

20 25 30

ctc aaa ggg ttg gct ctg gct ggt ctg att gga tca gcc tgg ctg ctc 144
 Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu
 35 40 45

tcc ctg ggc ctg agc tac acc ctg cca ctt gat cag acg cct ggg ctg 192
 Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu
 50 55 60

ttg att ggc agc ttg att ctg tgg cag acc ttt ctg cac acc ggg ctg 240
 Leu Ile Gly Ser Leu Ile Leu Trp Gln Thr Phe Leu His Thr Gly Leu
 65 70 75 80

ttc atc gtt gcc cac gat tcc atg cac gcc agt ctg gtt ccg ggt cat 288
 Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His
 85 90 95

ccc gga ttg aac cgc tgg atc ggc aaa gtg tat ttg ttg gtg tat gca 336
 Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala
 100 105 110

ggc ttg tct tat gag cgt tgt tcc cgc aac cac aga cgt cat cac ctg 384
 Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu
 115 120 125

gca ccg gag acg ttc cag gat cct gac tac caa cgt tgc acc aat aac 432
 Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn
 130 135 140

aac atc cta gat tgg tat gtt cac ttc atg ggc aac tat ctg ggc atg 480
 Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met
 145 150 155 160

cgg caa ctg tta aat cta agc tgt ctt tgg ctg gcg cta atc att ctc 528
 Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu
 165 170 175

aac ggt tct gat ctc cct gct cag atc atg cat ctg ctg ttg ttc agc 576
 Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser
 180 185 190

gtt ctg ccg ttg atc atc agt tcc tgt caa ttg ttt cta gtg gga acc 624
Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr
195 200 205

tgg tta ccc cac cga cgt ggg gcc acg aca cga ccg ggc gtg aca acg 672
Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr
210 215 220

cgc agc ctg gct ttg cat cca gcc ctc tct ttc gca gct tgt tac aac 720
Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn
225 230 235 240

ttt ggc tat cat cgt gaa cat cat gaa tcg cct tcc aca ccc tgg ttt 768
Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe
245 250 255

cag ctg cca caa ctt cga aat gaa tca ttc act tga 804
Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr
260 265

<210> 49
<211> 267
<212> PRT
<213> Unknown

<220>
<223> Artificial variant

<400> 49

Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His
1 5 10 15

Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala
20 25 30

Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu
35 40 45

Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu
50 55 60

Leu Ile Gly Ser Leu Ile Leu Trp Gln Thr Phe Leu His Thr Gly Leu
65 70 75 80

Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His
85 90 95

Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala
100 105 110

Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu
115 120 125

Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn
130 135 140

Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met
 145 150 155 160
 Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu
 165 170 175
 Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser
 180 185 190
 Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr
 195 200 205
 Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr
 210 215 220
 Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn
 225 230 235 240
 Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe
 245 250 255
 Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr
 260 265

<210> 50
 <211> 804
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <223> Artificial variant

<400> 50
 atg aaa acg aca aga tct att tcg tgg cca tcg act tgc tgg cat cac 48
 Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His
 1 5 10 15
 cag ccg agt tgc tca agc tgg gtg gca aat gag ttc agc cct cag gcc 96
 Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala
 20 25 30
 ctc aaa ggg ttg gct ctg gct ggt ctg att gga tca gcc tgg ctg ctc 144
 Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu
 35 40 45
 tcc ctg ggc ctg agc tac acc ctg cca ctt gat cag acg cct ggg ctg 192
 Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu
 50 55 60
 ttg att ggc agc ttg att ctg ctc aga gca ttt ctg cac acc ggg ctg 240
 Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu
 65 70 75 80
 ttc atc gtt gcc cac gat tcc atg cac gcc agt ctg gtt ccg ggt cat 288
 Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His
 85 90 95

ccc gga ttg aac cgc tgg atc ggc aaa gtg tat ttg ttg gtg tat gca 336
 Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala
 100 105 110

ggc ttg tct tat gag cgt tgt tcc cgc aac cac aga cgt cat cac gga 384
 Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Gly
 115 120 125

cat cct ggt act gat tta gat cct gac tac caa cgt tgc acc aat aac 432
 His Pro Gly Thr Asp Leu Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn
 130 135 140

aac atc cta gat tgg tat gtt cac ttc atg ggc aac tat ctg ggc atg 480
 Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met
 145 150 155 160

cgg caa ctg tta aat cta agc tgt ctt tgg ctg gcg cta atc att ctc 528
 Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu
 165 170 175

aac ggt tct gat ctc cct gct cag atc atg cat ctg ctg ttg ttc agc 576
 Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser
 180 185 190

gtt ctg ccg ttg atc atc agt tcc tgt caa ttg ttt cta gtg gga acc 624
 Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr
 195 200 205

tgg tta ccc cac cga cgt ggg gcc acg aca cga ccg ggc gtg aca acg 672
 Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr
 210 215 220

cgc agc ctg gct ttg cat cca gcc ctc tct ttc gca gct tgt tac aac 720
 Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn
 225 230 235 240

ttt ggc tat cat cgt gaa cat cat gaa tcg cct tcc aca ccc tgg ttt 768
 Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe
 245 250 255

cag ctg cca caa ctt cga aat gaa tca ttc act tga 804
 Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr
 260 265

<210> 51
 <211> 267
 <212> PRT
 <213> Unknown

<220>
 <223> Artificial variant

<400> 51
 Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His
 1 5 10 15

Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala
 20 25 30
 Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu
 35 40 45
 Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu
 50 55 60
 Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu
 65 70 75 80
 Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His
 85 90 95
 Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala
 100 105 110
 Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Gly
 115 120 125
 His Pro Gly Thr Asp Leu Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn
 130 135 140
 Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met
 145 150 155 160
 Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu
 165 170 175
 Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser
 180 185 190
 Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr
 195 200 205
 Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr
 210 215 220
 Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn
 225 230 235 240
 Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe
 245 250 255
 Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr
 260 265

<210> 52
 <211> 690
 <212> DNA
 <213> Nodularia spumigena NSOR10

<220>
 <221> CDS

<400> 52

atg gcg atc gcc att att agt ata tgg gct atc agc cta ggt ttg tta	48
Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile Ser Leu Gly Leu Leu	
1 5 10 15	
ctt tat att gat ata tcc caa ttc aag ttt tgg atg ttg tta ccg ctc	96
Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu	
20 25 30	
ata ttt tgg caa aca ttt tta tat acg gga tta ttt att aca gct cat	144
Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His	
35 40 45	
gat gcc atg cat ggg gta gtt ttt ccc aaa aat ccc aaa atc aac cat	192
Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His	
50 55 60	
ttc att ggc tca ttg tgc ctg ttt ctt tat ggt ctt tta cct tat caa	240
Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln	
65 70 75 80	
aaa ctt tta aaa aag cat tgg cta cat cac cat aat cca gcc agt gaa	288
Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Glu	
85 90 95	
aca gat cca gat ttt cac aac ggg aag cag aaa aac ttt ttt gct tgg	336
Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp	
100 105 110	
tat tta tat ttt atg aag cgt tac tgg agt tgg tta caa att atc aca	384
Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu Gln Ile Ile Thr	
115 120 125	
tta atg att att tat aac tta cta aaa tat ata tgg cat ttt cca gag	432
Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp His Phe Pro Glu	
130 135 140	
gat aat atg act tat ttt tgg gta gtt ccc tca att tta agt tct tta	480
Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile Leu Ser Ser Leu	
145 150 155 160	
caa tta ttt tat ttt gga act ttt cta ccc cac agt gag cct gta gaa	528
Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Val Glu	
165 170 175	
ggt tat aaa gag cct cat cgt tcc caa act att agc cgt ccc att tgg	576
Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser Arg Pro Ile Trp	
180 185 190	
tgg tca ttt ata act tgt tac cat ttt ggt tat cat tac gaa cat cat	624
Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Tyr Glu His His	
195 200 205	
gaa tac ccc cat gtt cct tgg tgg caa tta cca gaa att tat aaa atg	672
Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu Ile Tyr Lys Met	
210 215 220	
tct aaa tca aat ttg tga	690

Ser Lys Ser Asn Leu
225

<210> 53
<211> 229
<212> PRT
<213> Nodularia spumigena NSOR10

<400> 53

Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile Ser Leu Gly Leu Leu
1 5 10 15

Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu
20 25 30

Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
35 40 45

Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His
50 55 60

Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln
65 70 75 80

Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Glu
85 90 95

Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp
100 105 110

Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu Gln Ile Ile Thr
115 120 125

Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp His Phe Pro Glu
130 135 140

Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile Leu Ser Ser Leu
145 150 155 160

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Val Glu
165 170 175

Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser Arg Pro Ile Trp
180 185 190

Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Tyr Glu His His
195 200 205

Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu Ile Tyr Lys Met
210 215 220

Ser Lys Ser Asn Leu
225

<210> 54
<211> 37

<212> DNA
 <213> Artificial sequence

<220>
 <223> Primer

<400> 54
 gcgc atg cat cta gaa atg atc cag tta gaa caa cca ctc agt cat caa

37

<210> 55
 <211> 37
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer

<400> 55
 gcgc atg ctc tag act attt tgctttgtaa atttctg

37

<210> 56
 <211> 792
 <212> DNA
 <213> Nostoc punctiforme ATCC 29133

<220>
 <221> CDS
 <222> (5)..(775)

<400> 56
 gcgc atg cat cta gaa atg atc cag tta gaa caa cca ctc agt cat caa 49
 Met His Leu Glu Met Ile Gln Leu Glu Gln Pro Leu Ser His Gln
 1 5 10 15

gca aaa ctg act cca gta ctg aga agt aaa tct cag ttt aag ggg ctt 97
 Ala Lys Leu Thr Pro Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu
 20 25 30

ttc att gct att gtc att gtt agc gca tgg gtc att agc ctg agt tta 145
 Phe Ile Ala Ile Val Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu
 35 40 45

tta ctt tcc ctt gac atc tca aag cta aaa ttt tgg atg tta ttg cct 193
 Leu Leu Ser Leu Asp Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro
 50 55 60

gtt ata cta tgg caa aca ttt tta tat acg gga tta ttt att aca tct 241
 Val Ile Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser
 65 70 75

cat gat gcc atg cat ggc gta gta ttt ccc caa aac acc aag att aat 289
 His Asp Ala Met His Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn
 80 85 90 95

cat ttg att gga aca ttg acc cta tcc ctt tat ggt ctt tta cca tat 337
 His Leu Ile Gly Thr Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr
 100 105 110

caa aaa cta ttg aaa aaa cat tgg tta cac cac cac aat cca gca agc 385
 Gln Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser
 115 120 125

tca ata gac ccg gat ttt cac aat ggt aaa cac caa agt ttc ttt gct 433
 Ser Ile Asp Pro Asp Phe His Asn Gly Lys His Gln Ser Phe Phe Ala
 130 135 140

tgg tat ttt cat ttt atg aaa ggt tac tgg agt tgg ggg caa ata att 481
 Trp Tyr Phe His Phe Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile
 145 150 155

gcg ttg act att att tat aac ttt gct aaa tac ata ctc cat atc cca 529
 Ala Leu Thr Ile Ile Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro
 160 165 170 175

agt gat aat cta act tac ttt tgg gtg cta ccc tcg ctt tta agt tca 577
 Ser Asp Asn Leu Thr Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser
 180 185 190

tta caa tta ttc tat ttt ggt act ttt tta ccc cat agt gaa cca ata 625
 Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile
 195 200 205

ggg ggt tat gtt cag cct cat tgt gcc caa aca att agc cgt cct att 673
 Gly Gly Tyr Val Gln Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile
 210 215 220

tgg tgg tca ttt atc acg tgc tat cat ttt ggc tac cac gag gaa cat 721
 Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Glu Glu His
 225 230 235

cac gaa tat cct cat att tct tgg tgg cag tta cca gaa att tac aaa 769
 His Glu Tyr Pro His Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys
 240 245 250 255

gca aaa tagtctagag catgcgc 792
 Ala Lys

<210> 57

<211> 257

<212> PRT

<213> Nostoc punctiforme ATCC 29133

<400> 57

Met His Leu Glu Met Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala
1 5 10 15

Lys Leu Thr Pro Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe
20 25 30

Ile Ala Ile Val Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu
35 40 45

Leu Ser Leu Asp Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val
50 55 60

Ile Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His
 65 70 75 80
 Asp Ala Met His Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His
 85 90 95
 Leu Ile Gly Thr Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln
 100 105 110
 Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Ser
 115 120 125
 Ile Asp Pro Asp Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp
 130 135 140
 Tyr Phe His Phe Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala
 145 150 155 160
 Leu Thr Ile Ile Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser
 165 170 175
 Asp Asn Leu Thr Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu
 180 185 190
 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly
 195 200 205
 Gly Tyr Val Gln Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp
 210 215 220
 Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His
 225 230 235 240
 Glu Tyr Pro His Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala
 245 250 255

Lys

<210> 58
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer

<400> 58
 gtcgaccctg ctttaatgag atatgc

26

<210> 59
 <211> 27
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer

<400> 59
ctcgagcttg gacaatcagt aaattga 27

<210> 60
<211> 210
<212> DNA
<213> Agrobacterium tumefaciens

<220>
<221> Terminator

<400> 60
gtcgaccctg ctttaatgag atatgcgaga cgccatgat cgcatgatat ttgctttcaa 60
ttctgttgtg cacgttgtaa aaaacctgag catgtgtagc tcagatcctt accgccggtt 120
tcggttcatt ctaatgaata tatcaccctg tactatcgta tttttatgaa taatattctc 180
cgttcaattt actgattgtc caagctcgag 210

<210> 61
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 61
cccgggaatt cttcattatt tcgattttga tttcgtg 37

<210> 62
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 62
aagcttggtt gatcagaaga agaagaagaa gatgaact 38

<210> 63
<211> 652
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> Promoter

<400> 63
cccgggaatt cttcattatt tcgattttga tttcgtgacc agcgaacgca gaataccttg 60
ttgtgtaata ctttaccctg gtaaatcaaa aacaaaaagg cttttgagct ttttgtagtt 120
gaatttctct ggctgatctt ttctgtacag attcatatat ctgcagagac gatatacttg 180
attatttgag cttcttttga actatttcgt gtaatttggg atgagagctc tatgtatgtg 240
tgtaaacctt gaagacaaca agaaaggtaa caagtgaggg agggatgact ccatgtcaaa 300
atagatgtca taagaggccc atcaataagt gcttgagccc attagctagc ccagtaacta 360

ccagattgtg	agatggatgt	gtgaacagtt	ttttttttga	tgtaggactg	aaatgtgaac	420
aacaggcgca	tgaaaggcta	aattaggaca	atgataagca	gaaataactt	atcctctcta	480
acacttggcc	tcacattgcc	cttcacacaa	tccacacaca	tccaatcaca	acctcatcat	540
atatctcccg	ctaattcttt	tttctttgat	cttttttttt	ttgcttatta	tttttttgac	600
tttgatctcc	catcagttca	totttcttct	cttcttctga	tcaaccaagc	tt	652

<210> 64
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer

<400> 64
 gagctctagc gcaatcttat gtggtacaa 29

<210> 65
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer

<400> 65
 aagcttttct tgaaagtaaa gattgagtc 29

<210> 66
 <211> 1773
 <212> DNA
 <213> Petunia hybrida

<220>
 <221> Promoter
 <222> (1)..(1773)

<400> 66
 gagctctagc gcaatcttat gtggtacaaa tcttgattag tcgggaaaaa atgatgtggc 60
 cctacaaatg gttggaggat gggagatttg gctctatcta gagttatgtg gttggtgaag 120
 catttggtta ctctctgctg tggtagtttg catatccaca ttgtctcctt ccacttttat 180
 gacaattacg tgaaagttat gggttgtttt gtctattttt gtctgaggcct ttcttttcct 240
 tccaggttgt tgaagatggg ccaattcgat tagaataatg ttttgagctt tagcatattc 300
 tctctcgttt acacgattat agtaataatg atataggatg acagaagttg acacataaat 360
 tttttattct ctccatttac tttaatccaa atctcaccta ccctaaactt ctttaatatg 420
 tattcaatag tctatccgag taaattgtaa atttaacaac cattgataat attgacacct 480
 actaacatat actagtaaag agaataattaa catggcacat ataatttgat gcaaaatgag 540
 tatgatgaaa tttaaaccca aaatctcttg attttgacag tgtcaccttg acttggttaac 600
 taataagtca tgtttttagtg gcagaaagac aaactcatcc accaactgta tagcaataaa 660
 aaatagaaga atcttctctga ggcaaagttt tggaaaaatt aagagtggct gagatttaaat 720
 ttcaacagga attagttcca cttaactttt aggttacgat acagtgcctaa ttaaataact 780
 taattgtatt agatatttct tgcacctaaa aaatttaaaa actgaaaaaa ggtagcaatc 840
 aaaataaaca aaaggacaaa ataagtgaag ggtacagcca ccaacctggg cggctcactg 900
 ttgtgttggtt aaaacgtaga cttacaccta ccaaaatcta caactaaaat gaggcaataa 960
 tactttgccc aaaattacca agaaaagaaa aagaaaggaa tcccttaata ttactctcct 1020
 ccatttcaca ataaatatcc tagtttgact taaattagag tttaaaaaat gaaagacgac 1080

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ttttaaaact tgtaatctaa aataaatcat agttaaatgt gtggctataa atcattgtat 1140
taacggtaaa gtggtaagtt taaaagttaa ttgttttcaa atataaaatt gtactatcat 1200
tctttttgga atggactaat aagaaaacta tgacatccat tatggagcgg agggagtatc 1260
tccttttaac aataaccttt gtcccttcaa ttcaattatc agtatgcaaa cattaataat 1320
tattattgat gttaagtacc acatcatcct taatgataga atcatcgtag aacgcttttc 1380
caggcacaca ttcaaactag ttagaccagt accacacatc gaatattcca gacttctttg 1440
tttgaatagt cgactacatt ggataatgga acttctcgaa ttaacttcga attagtcgag 1500
cccaaaataa tatatacgtc ggggtgaaaa ctataaaatg ttgacaaaa atgtcaaatt 1560
aatatatcaa tctgcaacaa ccttttcacc ttgagaacac agctgaaatt ttttaciaag 1620
gtagttggtg aagctagtca gogaatccca ttaccttcca ctctacctaa ccccttcac 1680
caacaacaaa tttctgtaat ttaaaaacta gccaaaaaag aactctcttt taaaagagc 1740
caaagactca atctttactt tcaagaaaag ctt 1773

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<210> 67
<211> 39
<212> DNA
<213> Artificial sequence

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<220>
<223> Primer

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<400> 67
gcgc atg cat cta gaa atg aat ttt tgt gat aaa cca gtt agc tat tat 39

```

```

<210> 68
<211> 37
<212> DNA
<213> Artificial sequence

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<220>
<223> Primer

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<400> 68
gcgc atgctc tagattacga attggttact gaattgt 37

```

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<210> 69
<211> 819
<212> DNA
<213> Nostoc punctiforme ATCC 29133

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<220>
<221> CDS
<222> (5)..(802)

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<400> 69
gcgc atg cat cta gaa atg aat ttt tgt gat aaa cca gtt agc tat tat 49
      Met His Leu Glu Met Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr
      1           5           10           15

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gtt gca ata gag caa tta agt gct aaa gaa gat act gtt tgg ggg ctg 97
Val Ala Ile Glu Gln Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu
      20           25           30

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gtg att gtc ata gta att att agt ctt tgg gta gct agt ttg gct ttt 145
Val Ile Val Ile Val Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe
      35           40           45

```

tta cta gct att aat tat gcc aaa gtc cca att tgg ttg ata cct att	193
Leu Leu Ala Ile Asn Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile	
50 55 60	
gca ata gtt tgg caa atg ttc ctt tat aca ggg cta ttt att act gca	241
Ala Ile Val Trp Gln Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala	
65 70 75	
cat gat gct atg cat ggg tca gtt tat cgt aaa aat ccc aaa att aat	289
His Asp Ala Met His Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn	
80 85 90 95	
aat ttt atc ggt tca cta gct gta gcg ctt tac gct gtg ttt cca tat	337
Asn Phe Ile Gly Ser Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr	
100 105 110	
caa cag atg tta aag aat cat tgc tta cat cat cgt cat cct gct agc	385
Gln Gln Met Leu Lys Asn His Cys Leu His His Arg His Pro Ala Ser	
115 120 125	
gaa gtt gac cca gat ttt cat gat ggt aag aga aca aac gct att ttc	433
Glu Val Asp Pro Asp Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe	
130 135 140	
tgg tat ctc cat ttc atg ata gaa tac tcc agt tgg caa cag tta ata	481
Trp Tyr Leu His Phe Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile	
145 150 155	
gta cta act atc cta ttt aat tta gct aaa tac gtt ttg cac atc cat	529
Val Leu Thr Ile Leu Phe Asn Leu Ala Lys Tyr Val Leu His Ile His	
160 165 170 175	
caa ata aat ctc atc tta ttt tgg agt att cct cca att tta agt tcc	577
Gln Ile Asn Leu Ile Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser	
180 185 190	
att caa ctg ttt tat ttc gga aca ttt ttg cct cat cga gaa ccc aag	625
Ile Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys	
195 200 205	
aaa gga tat gtt tat ccc cat tgc agc caa aca ata aaa ttg cca act	673
Lys Gly Tyr Val Tyr Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr	
210 215 220	
ttt ttg tca ttt atc gct tgc tac cac ttt ggt tat cat gaa gaa cat	721
Phe Leu Ser Phe Ile Ala Cys Tyr His Phe Gly Tyr His Glu Glu His	
225 230 235	
cat gag tat ccc cat gta cct tgg tgg caa ctt cca tct gta tat aag	769
His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys	
240 245 250 255	
cag aga gta ttc aac aat tca gta acc aat tcg taatctagag catgcgc	819
Gln Arg Val Phe Asn Asn Ser Val Thr Asn Ser	
260 265	

<210> 70
 <211> 266
 <212> PRT
 <213> Nostoc punctiforme ATCC 29133

<400> 70

Met	His	Leu	Glu	Met	Asn	Phe	Cys	Asp	Lys	Pro	Val	Ser	Tyr	Tyr	Val	1	5	10	15
Ala	Ile	Glu	Gln	Leu	Ser	Ala	Lys	Glu	Asp	Thr	Val	Trp	Gly	Leu	Val	20	25	30	
Ile	Val	Ile	Val	Ile	Ile	Ser	Leu	Trp	Val	Ala	Ser	Leu	Ala	Phe	Leu	35	40	45	
Leu	Ala	Ile	Asn	Tyr	Ala	Lys	Val	Pro	Ile	Trp	Leu	Ile	Pro	Ile	Ala	50	55	60	
Ile	Val	Trp	Gln	Met	Phe	Leu	Tyr	Thr	Gly	Leu	Phe	Ile	Thr	Ala	His	65	70	75	80
Asp	Ala	Met	His	Gly	Ser	Val	Tyr	Arg	Lys	Asn	Pro	Lys	Ile	Asn	Asn	85	90	95	
Phe	Ile	Gly	Ser	Leu	Ala	Val	Ala	Leu	Tyr	Ala	Val	Phe	Pro	Tyr	Gln	100	105	110	
Gln	Met	Leu	Lys	Asn	His	Cys	Leu	His	His	Arg	His	Pro	Ala	Ser	Glu	115	120	125	
Val	Asp	Pro	Asp	Phe	His	Asp	Gly	Lys	Arg	Thr	Asn	Ala	Ile	Phe	Trp	130	135	140	
Tyr	Leu	His	Phe	Met	Ile	Glu	Tyr	Ser	Ser	Trp	Gln	Gln	Leu	Ile	Val	145	150	155	160
Leu	Thr	Ile	Leu	Phe	Asn	Leu	Ala	Lys	Tyr	Val	Leu	His	Ile	His	Gln	165	170	175	
Ile	Asn	Leu	Ile	Leu	Phe	Trp	Ser	Ile	Pro	Pro	Ile	Leu	Ser	Ser	Ile	180	185	190	
Gln	Leu	Phe	Tyr	Phe	Gly	Thr	Phe	Leu	Pro	His	Arg	Glu	Pro	Lys	Lys	195	200	205	
Gly	Tyr	Val	Tyr	Pro	His	Cys	Ser	Gln	Thr	Ile	Lys	Leu	Pro	Thr	Phe	210	215	220	
Leu	Ser	Phe	Ile	Ala	Cys	Tyr	His	Phe	Gly	Tyr	His	Glu	Glu	His	His	225	230	235	240
Glu	Tyr	Pro	His	Val	Pro	Trp	Trp	Gln	Leu	Pro	Ser	Val	Tyr	Lys	Gln	245	250	255	
Arg	Val	Phe	Asn	Asn	Ser	Val	Thr	Asn	Ser	260	265								

<210> 71
 <211> 33
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer

<400> 71
 gcgcatgcat ctagaaatgg cgatcgccat tat 33

<210> 72
 <211> 32
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer

<400> 72
 gcgcatgctc tagatcacaa atttgattta ga 32

<210> 73
 <211> 720
 <212> DNA
 <213> Nodularia spumigena NSOR10

<220>
 <221> CDS
 <222> (5)..(703)

<400> 73
 gcgc atg cat cta gaa atg gcg atc gcc att att agt ata tgg gct atc 49
 Met His Leu Glu Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile
 1 5 10 15

agc cta ggt ttg tta ctt tat att gat ata tcc caa ttc aag ttt tgg 97
 Ser Leu Gly Leu Leu Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp
 20 25 30

atg ttg tta ccg ctc ata ttt tgg caa aca ttt tta tat acg gga tta 145
 Met Leu Leu Pro Leu Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu
 35 40 45

ttt att aca gct cat gat gcc atg cat ggg gta gtt ttt ccc aaa aat 193
 Phe Ile Thr Ala His Asp Ala Met His Gly Val Val Phe Pro Lys Asn
 50 55 60

ccc aaa atc aac cat ttc att ggc tca ttg tgc ctg ttt ctt tat ggt 241
 Pro Lys Ile Asn His Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly
 65 70 75

ctt tta cct tat caa aaa ctt tta aaa aag cat tgg cta cat cac cat 289
 Leu Leu Pro Tyr Gln Lys Leu Leu Lys Lys His Trp Leu His His His
 80 85 90 95

aat cca gcc agt gaa aca gat cca gat ttt cac aac ggg aag cag aaa 337
 Asn Pro Ala Ser Glu Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys
 100 105 110

aac ttt ttt gct tgg tat tta tat ttt atg aag cgt tac tgg agt tgg 385
 Asn Phe Phe Ala Trp Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp
 115 120 125

tta caa att atc aca tta atg att att tat aac tta cta aaa tat ata 433
 Leu Gln Ile Ile Thr Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile
 130 135 140

tgg cat ttt cca gag gat aat atg act tat ttt tgg gta gtt ccc tca 481
 Trp His Phe Pro Glu Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser
 145 150 155

att tta agt tct tta caa tta ttt tat ttt gga act ttt cta ccc cac 529
 Ile Leu Ser Ser Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His
 160 165 170 175

agt gag cct gta gaa ggt tat aaa gag cct cat cgt tcc caa act att 577
 Ser Glu Pro Val Glu Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile
 180 185 190

agc cgt ccc att tgg tgg tca ttt ata act tgt tac cat ttt ggt tat 625
 Ser Arg Pro Ile Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr
 195 200 205

cat tac gaa cat cat gaa tac ccc cat gtt cct tgg tgg caa tta cca 673
 His Tyr Glu His His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro
 210 215 220

gaa att tat aaa atg tct aaa tca aat ttg tgatctagag catgctgc 720
 Glu Ile Tyr Lys Met Ser Lys Ser Asn Leu
 225 230

<210> 74

<211> 233

<212> PRT

<213> Nodularia spumigena NSOR10

<400> 74

Met His Leu Glu Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile Ser
1 5 10 15

Leu Gly Leu Leu Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met
20 25 30

Leu Leu Pro Leu Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe
35 40 45

Ile Thr Ala His Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro
50 55 60

Lys Ile Asn His Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu
65 70 75 80

Leu Pro Tyr Gln Lys Leu Leu Lys Lys His Trp Leu His His His Asn

85					90					95					
Pro	Ala	Ser	Glu	Thr	Asp	Pro	Asp	Phe	His	Asn	Gly	Lys	Gln	Lys	Asn
			100					105					110		
Phe	Phe	Ala	Trp	Tyr	Leu	Tyr	Phe	Met	Lys	Arg	Tyr	Trp	Ser	Trp	Leu
			115					120					125		
Gln	Ile	Ile	Thr	Leu	Met	Ile	Ile	Tyr	Asn	Leu	Leu	Lys	Tyr	Ile	Trp
			130					135					140		
His	Phe	Pro	Glu	Asp	Asn	Met	Thr	Tyr	Phe	Trp	Val	Val	Pro	Ser	Ile
Leu	Ser	Ser	Leu	Gln	Leu	Phe	Tyr	Phe	Gly	Thr	Phe	Leu	Pro	His	Ser
				165					170					175	
Glu	Pro	Val	Glu	Gly	Tyr	Lys	Glu	Pro	His	Arg	Ser	Gln	Thr	Ile	Ser
				180					185					190	
Arg	Pro	Ile	Trp	Trp	Ser	Phe	Ile	Thr	Cys	Tyr	His	Phe	Gly	Tyr	His
				195					200					205	
Tyr	Glu	His	His	Glu	Tyr	Pro	His	Val	Pro	Trp	Trp	Gln	Leu	Pro	Glu
				210					215					220	
Ile	Tyr	Lys	Met	Ser	Lys	Ser	Asn	Leu							
				225				230							

<210> 75
 <211> 258
 <212> DNA
 <213> Unknown

<220>
 <223> Nucleic acid sequence cassette containing the plastid transit peptide of the tobacco plastic transketolase

<400>	75	
ggtaccatgg	cgtcttcttc	ttctctcact
cctcgccatg	gctctgcctc	ttcttctcaa
cttaaatacca	atcccaatat	caccacctcc
gccgccgtcg	taaggtcacc	ggcgattcgt
actgagactg	cgggatcc	
		60
		120
		180
		240
		258

<210> 76
 <211> 260
 <212> DNA
 <213> Unknown

<220>
 <223> Nucleic acid sequence cassette containing the plastid transit peptide of the tobacco plastic transketolase

<400>	76	
ggtaccatgg	cgtcttcttc	ttctctcact
cctcgccatg	gctctgcctc	ttcttctcaa
		60
		120

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cttaaatcca atcccaatat caccacctcc cgccgccgta ctcttctctc cgccgccgcc 180
gccgccgtcg taaggtcacc ggcgattcgt gcctcagctg caaccgaaac catagagaaa 240
actgagactg cgctggatcc                                     260

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<210> 77
<211> 259
<212> DNA
<213> Unknown

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<220>

<223> Nucleic acid sequence cassette containing the plastid transit peptide of the tobacco plastic transketolase

<400> 77

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cttaaatcca atcccaatat caccacctcc cgccgccgta ctcttctctc cgccgccgcc 180
gccgccgtcg taaggtcacc ggcgattcgt gcctcagctg caaccgaaac catagagaaa 240
actgagactg cggggatcc                                     259

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<210> 78
<211> 4
<212> PRT
<213> Unknown

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<220>

<223> Natural amino acid sequence of the N terminus of GGPP synthase (AF120272)

<400> 78

Met Leu Lys Glu
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<210> 79
<211> 10
<212> PRT
<213> Unknown

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<220>

<223> Altered amino acid sequence of the N terminus of GGPP synthase (AF120272)

<400> 79

Met Thr Pro Gln Thr Ala Met Val Lys Glu
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<210> 80
<211> 22
<212> DNA
<213> Unknown

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<220>

<223> Antisense-specific primer PR1

<400> 80
gcaagctcga cagctacaaa cc 22

<210> 81
<211> 24
<212> DNA
<213> Unknown

<220>
<223> Sense-specific primer PR2

<400> 81
gaagcatgca gctagcagcg acag 24

<210> 82
<211> 1155
<212> DNA
<213> Unknown

<220>
<223> PCR amplification fragment with PR1 and PR2 primers

<400> 82
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